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OM protein - protein search, using sw model

Run on: October 5, 2005, 11:14:40 ; Search time 24 Seconds
(without alignments)
2376.329 Million cell updates/sec

Title: US-09-445-614B-2
Perfect score: 4004
Sequence: 1 MTSPPSSPVRLTLDGGQE.....EEDGASENYPVQLQSN 764

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4004	100.0	764	3	US-09-235-451-36
2	4004	100.0	764	4	US-09-978-303-36
3	3988.5	99.6	889	4	US-09-132-316-2
4	3051.5	76.2	761	3	US-09-235-451-4
5	3051.5	76.2	761	3	US-09-978-303-4
6	3036.5	75.8	727	3	US-09-235-451-23
7	3036.5	75.8	727	4	US-09-978-303-23
8	1689	42.2	843	3	US-09-235-451-25
9	1689	42.2	843	4	US-09-978-303-25
10	1652	41.3	838	3	US-09-235-451-2
11	1652	41.3	838	4	US-09-132-316-3
12	1652	41.3	838	4	US-09-667-422-9
13	1652	41.3	838	4	US-09-978-303-2
14	1651.5	41.2	839	4	US-09-667-422-4
15	1645.5	41.1	839	3	US-09-197-636-2
16	1644.5	41.1	839	3	US-09-197-636-8
17	1644.5	41.1	839	3	US-09-235-451-34
18	1644.5	41.1	839	4	US-09-978-303-34
19	1639.5	40.9	839	4	US-09-533-220A-2
20	1639.5	40.9	839	4	US-09-949-016-6937
21	1638.5	40.9	839	3	US-09-197-636-4
22	1486	37.1	798	4	US-09-949-016-9926
23	1471	36.7	871	4	US-09-500-123-7
24	1440	36.0	279	4	US-09-149-476-500
25	1298.5	32.4	742	4	US-09-500-123-12
26	1281	32.0	811	4	US-09-500-123-9
27	969	24.2	511	4	US-09-667-422-5

28	634	15.8	725	4	US-09-350-457A-2	Sequence 2, Appli
29	607.5	15.2	727	4	US-09-350-457A-4	Sequence 4, Appli
30	430.5	10.8	511	4	US-09-759-143-909	Sequence 909, App
31	274	6.8	57	3	US-09-235-451-15	Sequence 15, Appl
32	274	6.8	57	4	US-09-978-303-15	Sequence 15, Appl
33	272	6.8	232	4	US-09-149-476-623	Sequence 623, App
34	247	6.2	71	3	US-09-235-451-14	Sequence 14, Appl
35	247	6.2	71	4	US-09-978-303-14	Sequence 6, Appli
36	225	5.6	1709	4	US-09-392-812A-6	Sequence 9882, Ap
37	223.5	5.6	978	4	US-09-949-016-9882	Sequence 11563, A
38	215	5.4	974	4	US-09-949-016-11563	Sequence 4, Appli
39	212.5	5.3	1619	4	US-09-392-812A-4	Sequence 2, Appli
40	190.5	4.8	1704	4	US-09-392-812A-2	Sequence 910, App
41	179	4.5	134	4	US-09-759-143-910	Sequence 6340, Ap
42	168.5	4.2	759	4	US-09-949-016-6340	Sequence 4, Appli
43	151	3.8	1839	2	US-09-172-977-4	Sequence 4, Appli
44	151	3.8	1839	4	US-09-404-108-4	Sequence 4, Appli
45	151	3.8	2753	4	US-09-949-016-7659	Sequence 7659, Ap

ALIGNMENTS

RESULT 1

US-09-235-451-36
; Sequence 36, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-235-451-36

Query Match	100.0%;	Score	4004;	DB	3;	Length	764;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	764;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MTSPSSPVRLTLDGGQSGSEARGKLDGSGGLPPMESQFGEDRKFAPIRVNLNY	60				
Db	1	MTSPSSPVRLTLDGGQSGSEARGKLDGSGGLPPMESQFGEDRKFAPIRVNLNY	60				
Qy	61	RKGTGASQDPNFRDRRLFNASRGVPEDLAGLPEYLSKTSKYLTDSEYEGSTGKTCL	120				
Db	61	RKGTGASQDPNFRDRRLFNASRGVPEDLAGLPEYLSKTSKYLTDSEYEGSTGKTCL	120				
Qy	121	MKAVLNKDGVNACILPLLQIDRDSGNPQLVNAQCTDDYYRGHSAHIAIEKRSLOCVK	180				
Db	121	MKAVLNKDGVNACILPLLQIDRDSGNPQLVNAQCTDDYYRGHSAHIAIEKRSLOCVK	180				
Qy	181	LLVENGANVHARACGRFFQKGQTCFYFGEPLSLAACTQMDVSVYLLNPHQPASLOA	240				
Db	181	LLVENGANVHARACGRFFQKGQTCFYFGEPLSLAACTQMDVSVYLLNPHQPASLOA	240				
Qy	241	TDGQNTVLHALVMSIDNSAENTALTSMYDGLQAGARLCPTVQLEDIRNLQDLTPKL	300				
Db	241	TDGQNTVLHALVMSIDNSAENTALTSMYDGLQAGARLCPTVQLEDIRNLQDLTPKL	300				
Qy	301	AAKEGKIEIFRHILQREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEANSVLEITAF	360				

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Db 301 AAKEGKIEIFRIHLQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIAF 360
QY 361 HCKSPHRHRMVLEPLNKLQAKWDLILPKPFFLNFLCNLIYMPIFTAVAYHOPTLKKQAA 420
Db 361 HCKSPHRHRMVLEPLNKLQAKWDLILPKPFFLNFLCNLIYMPIFTAVAYHOPTLKKQAA 420
QY 421 PHLKAEGVNSMLLTGHILILGGIYLLVGQWVFWRRHVFIWISFIDSYFEILFLFOALL 480
Db 421 PHLKAEGVNSMLLTGHILILGGIYLLVGQWVFWRRHVFIWISFIDSYFEILFLFOALL 480
QY 481 TVVSQVLCFLAEWYLPVLVSALVGLWMLLYYTRGFQHTGIYSVMIQKVILRDLRLFL 540
Db 481 TVVSQVLCFLAEWYLPVLVSALVGLWMLLYYTRGFQHTGIYSVMIQKVILRDLRLFL 540
QY 541 IYLVFLFGFAVALVSLSQEAWRPEPTGPNATESVQMEQDEGNGAQYRGILEASLEL 600
Db 541 IYLVFLFGFAVALVSLSQEAWRPEPTGPNATESVQMEQDEGNGAQYRGILEASLEL 600
QY 601 FKPTIGMGLAFQEOQLHFRGMVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660
Db 601 FKPTIGMGLAFQEOQLHFRGMVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660
QY 661 KLQKALSVLEMENGYWCKKQKORAGVMLTVGTPDGSPPERWCFRVEEVNWNASWEQTLPT 720
Db 661 KLQKALSVLEMENGYWCKKQKORAGVMLTVGTPDGSPPERWCFRVEEVNWNASWEQTLPT 720
QY 721 LCEDPSGAGVPRTELENPVLASPPKEDGEGASENYYVPVQLQSN 764
Db 721 LCEDPSGAGVPRTELENPVLASPPKEDGEGASENYYVPVQLQSN 764

RESULT 2
US-09-978-303-36
; Sequence 36, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-303-36

Query Match 100.0%; Score 4004; DB 4; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPSSPPVRLTLDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFPAPQIRVNLNY 60
Db 1 MTSPSSPPVRLTLDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFPAPQIRVNLNY 60
QY 61 RKGTSAGQDPNRFDRDLRFLNFAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
Db 61 RKGTSAGQDPNRFDRDLRFLNFAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
QY 121 MKAVNLKDGVNACILPLLQIDRDSGNPQLVNAQCTDDYYRGHSALHIAIEKRSIQCVK 180
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Db 121 MKAVNLKDGVNACILPLLQIDRDSGNPQLVNAQCTDDYYRGHSALHIAIEKRSIQCVK 180
QY 181 LLVENGANVHARACGRFPQKGGTCFYFGELPLSLAACTKQWDVSYLLENPHQASLOA 240
Db 181 LLVENGANVHARACGRFPQKGGTCFYFGELPLSLAACTKQWDVSYLLENPHQASLOA 240
QY 241 TDSQGNTVLHALVMSDNSAENIALVTSMYDGLQAGARLCTPQVLEDIRNLQDLTPLKL 300
Db 241 TDSQGNTVLHALVMSDNSAENIALVTSMYDGLQAGARLCTPQVLEDIRNLQDLTPLKL 300
QY 301 AAKEGKIEIFRIHLQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIAF 360
Db 301 AAKEGKIEIFRIHLQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIAF 360
QY 361 HCKSPHRHRMVLEPLNKLQAKWDLILPKPFFLNFLCNLIYMPIFTAVAYHOPTLKKQAA 420
Db 361 HCKSPHRHRMVLEPLNKLQAKWDLILPKPFFLNFLCNLIYMPIFTAVAYHOPTLKKQAA 420
QY 421 PHLKAEGVNSMLLTGHILILGGIYLLVGQWVFWRRHVFIWISFIDSYFEILFLFOALL 480
Db 421 PHLKAEGVNSMLLTGHILILGGIYLLVGQWVFWRRHVFIWISFIDSYFEILFLFOALL 480
QY 481 TVVSQVLCFLAEWYLPVLVSALVGLWMLLYYTRGFQHTGIYSVMIQKVILRDLRLFL 540
Db 481 TVVSQVLCFLAEWYLPVLVSALVGLWMLLYYTRGFQHTGIYSVMIQKVILRDLRLFL 540
QY 541 IYLVFLFGFAVALVSLSQEAWRPEPTGPNATESVQMEQDEGNGAQYRGILEASLEL 600
Db 541 IYLVFLFGFAVALVSLSQEAWRPEPTGPNATESVQMEQDEGNGAQYRGILEASLEL 600
QY 601 FKPTIGMGLAFQEOQLHFRGMVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660
Db 601 FKPTIGMGLAFQEOQLHFRGMVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660
QY 661 KLQKALSVLEMENGYWCKKQKORAGVMLTVGTPDGSPPERWCFRVEEVNWNASWEQTLPT 720
Db 661 KLQKALSVLEMENGYWCKKQKORAGVMLTVGTPDGSPPERWCFRVEEVNWNASWEQTLPT 720
QY 721 LCEDPSGAGVPRTELENPVLASPPKEDGEGASENYYVPVQLQSN 764
Db 721 LCEDPSGAGVPRTELENPVLASPPKEDGEGASENYYVPVQLQSN 764

RESULT 3
US-09-132-316-2
; Sequence 2, Application US/09132316B
; Patent No. 6444440
; GENERAL INFORMATION:
; APPLICANT: Young, Paul E.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Vanilloid Receptor-2
; FILE REFERENCE: 1488.1110000
; CURRENT APPLICATION NUMBER: US/09/132,316B
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: US 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 889
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-132-316-2

Query Match 99.6%; Score 3988.5; DB 4; Length 889;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 763; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MTSPSSPPVRLTLDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFPAPQIRVNLNY 60
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Db 127 MTSPPSSPVFRLETTLDGGQDGEADRGKLDGSGLPMPMESQFQGEDRKFAFQIRVNLNY 186
QY 61 RKGATGASQDPPNRFRDRRLFNVAISRGVDPEDLAGLPEYLSKTSKYLTDSEYTGSGTKTCL 120
Db 187 RKGATGASQDPPNRFRDRRLFNVAISRGVDPEDLAGLPEYLSKTSKYLTDSEYTGSGTKTCL 246
QY 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYVYRHSALHIAIEKRSIQCVK 180
Db 247 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYVYRHSALHIAIEKRSIQCVK 306
QY 181 LLVANGANVHARACGRFFQKQGTCTFYFGBELPLSLAACTKQWDVSVYLLLENPHQASLOA 240
Db 307 LLVANGANVHARACGRFFQKQGTCTFYFGBELPLSLAACTKQWDVSVYLLLENPHQASLOA 366
QY 241 TDSQGNVTLHALVMIADNSAENIALVTSMYDGLLQAGARLCPVTQVLEDIRNLQDITPLKL 300
Db 367 TDSQGNVTLHALVMIADNSAENIALVTSMYDGLLQAGARLCPVTQVLEDIRNLQDITPLKL 426
QY 301 AAKEGKIEIFRHILOREFSGLSHRKFTWCYGPVRVSYLDLASVDSCEENSVLIEIAP 360
Db 427 AAKEGKIEIFRHILOREFSGLSHRKFTWCYGPVRVSYLDLASVDSCEENSVLIEIAP 486
QY 361 HCKSPHRHRMVLEPLNKLQAKWDLIIPKFFLNFLCNLIYMFIFTAVAYHQTPLKQAA 420
Db 487 HCKSPHRHRMVLEPLNKLQAKWDLIIPKFFLNFLCNLIYMFIFTAVAYHQTPLKQAA 545
QY 421 PHLKAEGVNSMLTGHILILGIGIYLLVQGLWYFWRHRVFIWISFIDSYSFEILF 480
Db 546 PHLKAEGVNSMLTGHILILGIGIYLLVQGLWYFWRHRVFIWISFIDSYSFEILF 605
QY 481 TVVSQVLCFLAIEWYPLNLSALVGLWNLNLYYTRGFQHTGIYSVMIOKVILRDLRFL 540
Db 606 TVVSQVLCFLAIEWYPLNLSALVGLWNLNLYYTRGFQHTGIYSVMIOKVILRDLRFL 665
QY 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEQDEGNGAQYRGILEASLEL 600
Db 666 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEQDEGNGAQYRGILEASLEL 725
QY 601 FKFTIGMELAFQELHFRGMVLLLLAYVLLTYLLNMLNLIAMSETVNSVATDSWSIW 660
Db 726 FKFTIGMELAFQELHFRGMVLLLLAYVLLTYLLNMLNLIAMSETVNSVATDSWSIW 785
QY 661 KLOKATSVLEWENGYWCRKQKQAGVMLTVGTPDGSPPDERWCFRVEEVNWSWEOQLPT 720
Db 786 KLOKATSVLEWENGYWCRKQKQAGVMLTVGTPDGSPPDERWCFRVEEVNWSWEOQLPT 845
QY 721 LCEDPGAGVPRTLNENPVLASPPKEDGEGASEENYVPVQLQSN 764
Db 846 LCEDPGAGVPRTLNENPVLASPPKEDGEGASEENYVPVQLQSN 889

RESULT 4
US-09-235-451-4
; Sequence 4, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 761
; TYPE: PRT

; ORGANISM: R. rattus
US-09-235-451-4
Query Match 76.2%; Score 3051.5; DB 3; Length 761;
Best Local Similarity 77.7%; Pred. No. 1.9e-278; Indels 17; Gaps 7;
Matches 598; Conservative 62; Mismatches 93;
QY 1 MTSPPSSPVFRLETTLDGGQDGEADRGKLDGSGLPMPMESQFQGEDRKFAFQIRVNLNY 60
Db 1 MTSASPPAFRLETSDEEGNAEVNKGQE----PPMPESPQREDRNSSPQIKVNLNF 56
QY 61 ----RKGTA--SQDPPNRPDRRLFNVAISRGVDPEDLAGLPEYLSKTSKYLTDSEYTGSGT 115
Db 57 IKRPKNTSAPSQDPPDRDRDLFNVSRGVSPPELTGLLEYLRWNSKYLTDSEYTGSGT 116
QY 116 GKTCLMKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYVYRHSALHIAIEKRS 175
Db 117 GKTCLMKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYVYRHSALHIAIEKRS 176
QY 176 LQCVKLLVANGANVHARACGRFFQKQGTCTFYFGBELPLSLAACTKQWDVSVYLLLENPHQ 235
Db 177 LQCVKLLVANGANVHARACGRFFQKQGTCTFYFGBELPLSLAACTKQWDVSVYLLLENPHQ 236
QY 236 ASLQATDSQNTVTLHALVMIADNSAENIALVTSMYDGLLQAGARLCPVTQVLEDIRNLQD 295
Db 237 ASLEATDSLGNTVTLHALVMIADNSAENIALVTSMYDGLLQAGARLCPVTQVLEDIRNLQD 296
QY 296 TPLKAAEGKIEIFRHILOREFSG--LSHLRKFTEWCYGPVRVSYLDLASVDSCEENS 354
Db 297 TPLKAAEGKIEIFRHILOREFSGYQPLSRKFTWCYGPVRVSYLDLASVDSCEENS 356
QY 355 LEIIAFCHCKSPHRHRMVLEPLNKLQAKWDLIIPKFFLNFLCNLIYMFIFTAVAYHQT 414
Db 357 LEIIAFCHCKSPHRHRMVLEPLNKLQAKWDLIIPKFFLNFLCNLIYMFIFTAVAYHQS 416
QY 415 LKKQAAPHKAEVNSMLTGHILILGIGIYLLVQGLWYFWRHRVFIWISFIDSYSFEILF 474
Db 417 LQDPAIPSSKATFGESMLLGHILILGIGIYLLVQGLWYFWRHRVFIWISFIDSYSFEILF 476
QY 475 LQDPAIPSSKATFGESMLLGHILILGIGIYLLVQGLWYFWRHRVFIWISFIDSYSFEILF 534
Db 477 LQDPAIPSSKATFGESMLLGHILILGIGIYLLVQGLWYFWRHRVFIWISFIDSYSFEILF 536
QY 535 LRLFLIYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEQDEGNGAQYRGIL 594
Db 537 LRLFLIYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEQDEGNGAQYRGIL 594
QY 595 EASLELFKFTIGMELAFQELHFRGMVLLLLAYVLLTYLLNMLNLIAMSETVNSVAT 654
Db 595 DASLELFKFTIGMELAFQELHFRGMVLLLLAYVLLTYLLNMLNLIAMSETVNSVAT 654
QY 655 DSWSIWKLQKATSVLEWENGYWCRKQKQAGVMLTVGTPDGSPPDERWCFRVEEVNWS 713
Db 655 NWSIWKLOKATSVLEWENGYWCRKQKQAGVMLTVGTPDGSPPDERWCFRVEEVNWS 714
QY 714 WEOTPLTCEDPGAGVPRTLNENPVLASPPKEDGEGASEENYVPVQLQSN 763
Db 715 WEOTPLTCEDPGAGVPRTLNENPVLASPPKEDGEGASEENYVPVQLQSN 760

RESULT 5
US-09-978-303-4
; Sequence 4, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303

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; CURRENT FILLING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILLING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILLING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILLING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 761
; TYPE: PRT
; ORGANISM: R. rattus
US-09-978-303--4

Query Match 76.2%; Score 3051.5; DB 4; Length 761;
Best Local Similarity 77.7%; Pred. No. 1.9e-278;
Matches 598; Conservative 62; Mismatches 93; Indels 17; Gaps 7;

QY 1 MTSPPSSPVRLTLDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFAFQIRVNLNY 60
Db 1 MTSASSPPAPRLTSDGDEAGNAEVNKGQE-----PPMESPPQREDRNSSPQIKVNLNF 56

QY 61 ----RKG TGA-SQPDNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGST 115
Db 57 IKPPKNTSAPSOQEDRFDRDLFNAVSRGVPEELTGLLEYLRWNSKYLTDSEYTEGST 116

QY 116 GKTCMKAVLNKXGQVNAACILPLQLIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRS 175
Db 117 GKTCMKAVLNKXGQVNAACILPLQLIDKDSGNPKPLVNAQCTDEFFYQGHSAHIAIEKRS 176

QY 176 LQCVKLLVNGANVHARACGRPFQKGCTCFYFGELPLSLAACTKQWDVVSYLENPHOP 235
Db 177 LQCVKLLVNGADVHLRACGRPFQKGCTCFYFGELPLSLAACTKQWDVVSYLENPHOP 236

QY 236 ASLQATDSQNTVLHVLVMI SDNSAENIALVTSMYDGLLQAGARLCTPTQVLEDIRNLQDL 295
Db 237 ASLEATDSLNTVLHVLVMI SDNSAENIALVTSMYDGLLQAGARLCTPTQVLEIRSHOGL 296

QY 296 TPLKAAKEGKIEIFRHILQREFSG-LSHLSRKFTWCYGPVRVSLYDLASVDSCENSV 354
Db 297 TPLKAAKEGKIEIFRHILQREFSGVPQPLSRKFTWCYGPVRVSLYDLSSVDSWEKNSV 356

QY 355 LEIIAFCKSPHRHVMVLEPLNKLQAKWDLLI PKFPLNCLNLYMFIFTAVAYHOPT 414
Db 357 LEIIAFCKSPHRHVMVLEPLNKLQEKWDRLVSRFPFNFCYLYVMFTFTVAYHOQS 416

QY 415 LKQAAPHLKAEGVNSMLTGHILLLGGIYLLVGLWYFWRHVRFTWISFIDSYPEILF 474
Db 417 LDQPAIPSSKATFGESMLLGHILLLGGIYLLVGLWYFWRRLFTWISFIDSYPEILF 476

QY 475 LFOALLTWSQVLCFLAIEWYLPVLSALVGLNLLYYTRGFQHTGIYSVMTQKVILRD 534
Db 477 LQALLTVLSQVLRFMETEWYLPVLSVGLVGLNLLYYTRGFQHTGIYSVMTQKVILRD 536

QY 535 LIRPLLIYVLPFGFAVALVLSQEAWRPEAPTPGNATESVQMEQDEGNAQYRGIL 594
Db 537 LIRPLLIYVLPFGFAVALVLSREARSPKAPEDNNSVTVEQTPVQGEES--PAPYRSIL 594

QY 595 EASLELPKFTTGMGELAFQBLFRGMVLLLLAYLLVLLTLLNMLIALMSTVNSVAT 654
Db 595 DASLELPKFTTGMGELAFQBLFRGMVLLLLAYLLVLLTLLNMLIALMSTVNHAD 654

QY 655 DWSIWKLOKAI SVLEMENGYWC-RKQKQAGVMTVTGTPKDGSPDERWCFRVEEVNWA 713
Db 655 NWSIWKLOKAI SVLEMENGYWCCRKKHREGRLLVKVGTRGDGTPDERWCFRVEEVNWA 714

QY 714 WEOTLPTLCDDPSGVPRTLNPVPLASPKPEDEGASENYPVQLQOS 763
Db 715 WEKTLPTLSBDSGPGTGNKNPT-----SKPGKNSASEEDHLPQLVQLQOS 760

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US-09-235-451-23
; Sequence 23, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 727
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(727)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-235-451-23

Query Match 75.8%; Score 3036.5; DB 3; Length 727;
Best Local Similarity 79.1%; Pred. No. 4.6e-277;
Matches 620; Conservative 5; Mismatches 82; Indels 77; Gaps 10;

QY 1 MTSPPSSPVRLTLDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFAFQIRVNLNY 60
Db 1 MTSPPSSPVRLTLDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFAFQIRVNLNY 60

QY 61 RGTGASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSGTKTCL 120
Db 61 RGTGASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSGTKTCL 120

QY 121 MKAVLNKXGQVNAACILPLQLIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSIQCVK 180
Db 121 MKAVLNKXGQVNAACILPLQLIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSIQCVK 180

QY 181 LLVNGANVHARACGRPFQKGCTCFYFGELPLSLAACTKQWDVVSYLENPHOPASLOA 240
Db 181 LLVNGANVHARACGRPFQKGCTCFYFGELPLSLAACTKQWDVVSYLENPHOPASLOA 240

QY 241 TDSQNTVLHVLVMI SDNSAENIALVTSMYDGLLQAGARLCTPTQVLEDIRNLQDLTPLKL 300
Db 241 TDSQNTVLHVLVMI SDNSAENIALVTSMYDGLLQAGARLCTPTQVLEDIRNLQDLTPLKL 300

QY 301 AAKEGKIEIF-RHIL-QREFSGLS-HLSRKFTF-MCYGPVRVSLYDLASVDSCENSVLE 356
Db 301 AAKEGKIXIFXRHILASGKFLGPKPPFRKFTWMLMGVPRVXXXXXXXXXXXXXXXXXXXX 360

QY 357 IIAFHCKSPHRHVMVLEPLNKLQAKWDLLI PKFPLNCLNLYMFIFTAVAYHOPTLK 416
Db 361 XXXXXXXXDRHVMVLEPLNKLQAKWDLLI PKFPLNCLNLYMFIFTAVAYHOPTLK 420

QY 417 KQAAAPHLKAEGVNSMLTGHILLLGGIYLLVGLWYFWRHVRFTWISFIDSYPEILF 460
Db 421 KQAAAPHLKAEGVNSMLTGHILLLGGIYLLVGLWYFWRHVRFTWISFIDSYPEILF 478

QY 461 IWSIFDYSFEILFLFQALLTVVSQVLCFLAIEWYLPVLSALVGLNLLYYTRGFQHT 520
Db 479 -----RVVPAPACVCA---GAGLAEPALLYTWL-----PAHREL 509

QY 521 GIYSVMTQKVILRDLLRFLIYLVLPFGFAVALVLSQEAWRPEAPTPGNATESVQPMEG 580
Db 510 QCHD-----PEALVLSQD-WRPEAPTPGNATESVQPMEG 543

QY 581 QDEGNGAQYRGILKEASLELPKFTTGMGELAFQBLFRGMVLLLLAYLLVLLTLLNML 640

```


Db 544 QDEGNGAQRGILXASLELFKFTTGMGELAQEQQLHFRGMVLLLLAYVLLTYILLNM 603
Qy 641 LIALMSETVNSVATDSWSIWKLQKALSVLEMENGYWCRKQKORAGVMLTVGTPKPGSPDE 700
Db 604 LIALXSETVNSVATDSWSIWKLQKALSVLEMENGYWCRKQKORAGVMLTVGTPKPGSPDE 663
Qy 701 RWCFRVEEVNWSWETLPTLCEDPGAGVPTLENPVLASPPKEDGASBNYVPVQL 760
Db 664 RWCFRVEEVNWSWETLPTLCEDPGAGVPTLENPVLASPPKEDGASBNYVPVQL 723
Qy 761 LQSN 764
Db 724 LQSN 727

RESULT 7
US-09-978-303-23
; Sequence 23, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 727
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(727)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-978-303-23

Query Match 75.8%; Score 3036.5; DB 4; Length 727;
Best Local Similarity 79.1%; Pred. No. 4.6e-277;
Matches 620; Conservative 5; Mismatches 82; Indels 77; Gaps 10;
Qy 1 MTSPSSGPFVRLTLDGQEDGSEADRGKLDGSGLPPEMESQFGEDRKFAPIRVNLNY 60
Db 1 MTSPSSGPFVRLTLDGQEDGSEADRGKLDGSGLPPEMESQFGEDRKFAPIRVNLNY 60
Qy 61 RKGTSQDPNRRDRRLFNAGRGVPEDLAGLPEYLSKTSKYLTSYETGSGTKCL 120
Db 61 RKGTSQDPNRRDRRLFNAGRGVPEDLAGLPEYLSKTSKYLTSYETGSGTKCL 120
Qy 121 MKAVLNKQGNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLOCVK 180
Db 121 MKAVLNKQGNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGHSALHIAIEKRSLOCVK 180
Qy 181 LLVENGANVHARACGRPFQKQGTCTFYGELPLSLAACTQKQWVSVYLLNPHQPASLOA 240
Db 181 LLVENGANVHARAXXXXXXXXXXXXXXXXXXGELPLSLAACTQKQWVSVYLLNPHQPASLOA 240
Qy 241 TDSQNTVLHALVMSDMSAENIALVTSMYDGLLQAGARLCTVQLEDIRNLQDLTPKL 300
Db 241 TDSQNTVLHALVMSDMSAENIALVTSMYDGLLQAGARLCTVQLEDIRNLQDLTPKL 300
Qy 301 AAKEGKTEIF-RHIL-QREFSGLS-HLSRKETE-WCYGPVRSVLYDLASVDSCENSVLE 356

Db 301 AAKEGKIXIFXRHILASGKFSGLKPPFPKRPTWMLMGFVRVXXXXXXXXXXXXXXXXXXXX 360
Qy 357 IIAFCKSPHRRMVVLPNKLQAKWDLLIPKFFLPLCNLIYMFIFTAVAYHPTLK 416
Db 361 XXXXXXXPDRHRMVVLPNKLQAKWDLLIPKFFLPLCNLIYMFIFTAVAYHPTLK 420
Qy 417 QQAAPHLKAEVGNMMLTGHILILGGLYLLVQLWYFWRR-----HVP 460
Db 421 QQAAPHLKAEVGNMMLTGHILILGGLYLLVQLWYFWRR-----HVP 478
Qy 461 IWSIFDSYFEILFQALLTVVSVQLCELAETENWLPVLSALVLCMLNLLYYTRGFQHT 520
Db 479 -----RVVPAPACVCA---GAGLAEPALLYTWL-----PAHRHL 509
Qy 521 GIYSVMIOKVLRLDLLRLLIYLVFLFGFAVALSVLSQEAWEAPRTPGNATESVQPMEG 580
Db 510 QCHD-----PEALVLSLQD-WRPEAPTGNATESVQPMEG 543
Qy 581 QDEGNGAQRGILXASLELFKFTTGMGELAQEQQLHFRGMVLLLLAYVLLTYILLNM 640
Db 544 QDEGNGAQRGILXASLELFKFTTGMGELAQEQQLHFRGMVLLLLAYVLLTYILLNM 603
Qy 641 LIALMSETVNSVATDSWSIWKLQKALSVLEMENGYWCRKQKORAGVMLTVGTPKPGSPDE 700
Db 604 LIALXSETVNSVATDSWSIWKLQKALSVLEMENGYWCRKQKORAGVMLTVGTPKPGSPDE 663
Qy 701 RWCFRVEEVNWSWETLPTLCEDPGAGVPTLENPVLASPPKEDGASEENYVPVQL 760
Db 664 RWCFRVEEVNWSWETLPTLCEDPGAGVPTLENPVLASPPKEDGASEENYVPVQL 723
Qy 761 LQSN 764
Db 724 LQSN 727

RESULT 8
US-09-235-451-25
; Sequence 25, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 843
; TYPE: PRT
; ORGANISM: chicken
US-09-235-451-25

Query Match 42.2%; Score 1689; DB 3; Length 843;
Best Local Similarity 47.2%; Pred. No. 6.4e-150;
Matches 358; Conservative 118; Mismatches 218; Indels 64; Gaps 12;
Qy 4 PSSSPVRLTLDGQEDGSEADRGKLDGSGLPPEMESQFGEDRKFAPIRVNLN 59
Db 49 PSKSNIF-----ARRGRFVMGDCDKMAPMDSFYQ-MDHLMAPSVIKPHAN 93
Qy 60 YRKG-----TCASQPDNRRDRRLFNAGRGVPEDLAGLPEYLSKTSKYLTD 108
Db 94 MERGKHLKLLSTDSITGCSKAPKFDYRRIRFQAVARGSTKDLDDLLLYLNRLLKHTDD 153

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QY 109 EYTEGSTGCTCKMLKAVLNKDGYNACILPLLQIQRDSDGNPQPLVNAQCTDDYYRGHSALH 168
Db 154 EFKEPETGKTCLLKAAMLNLDHGKNDITPLLLDIAKKTGTLKEFVNAYETDNYTKGQTALH 213
QY 169 IAIEKRSLOCVKLLVNGANVHARACGRFFQKQG--TCFYFGELPLSLAACTKQMDVWSY 227
Db 214 IAIERENMYLVKLLVQNGADVHARACGEFFRKIKGKPGFYFGELPLSLAACTNQLCIVKF 273
QY 228 LLENPHQASLOATDSQNTVLHALVMSDNSAENIALVTSMDGLLQAGARLCPTVQLE 287
Db 274 LLENPYQAADIAAEDSMGNMVLHTLVEIADNTKNTKFTVMNNILILGAKINPILKLE 333
QY 288 DIRNLQDLTPLKAAKEGKIEFRHILQREFSG--LSHLSRKFTWCYGPVRVSLYDLAS 345
Db 334 ELTNKKGLTPLTAAKTGKIGIPAYILRREIKDPCRHSRKFTWAYGPHVSSLYDLSC 393
QY 346 VDSCEBNSVLEIIAFHCKSPHRRMVVLEPLNKLQAKWDLLIPK--FFLNFLCNLIYMPI 404
Db 394 IDTCEKNSVLEIIAYSSETPNRHEMLLVPEPLNLLQDKWDRFVKHLFYFNFFVYAIHISI 453
QY 405 FTAVAYHOPTLKQAAAPH--LKAEVGNSMLLTGHILILGGIYLLVQGLWYFWRHVFIMI 463
Db 454 LTTAAAYRVPQKDGKPPFAFGHSTGEYFRVTGEILSVLGLYFFFRGIQYFVQRRPSLKT 513
QY 464 SFIDSYPEILFQALLTVVSOVLCLAEIEMVLPPLVLSALVGLMNLVYTRGFOHTGIY 523
Db 514 LIVDSYSEVLFVHSLLSVVLYFCQGLYVASMVFSALGWMANMLYTRGFOOMGIY 573
QY 524 SVMIOKVILRLRFLLIYLVFLGFAVALVSLSQEAWRPEAPTGNATESVQPMEGQBD 583
Db 574 SVMIAKMILRDLRCRFMFVLYVFLGFASTAVTLIED-----DNEGQDT 616
QY 584 EGN-----GAQYRGILEASLELFKFTTGMGELAFQBLHPRGMVLLLLAYVLL 632
Db 617 NSSEYARCSHTRKGRTSYNSLYYTCLLEFKFTTGMGDLFTENYRFSKVFLVLLVYL 676
QY 633 TYILLANMLIALMSETVNSVATDSIWKLOKAIISVLEMENGYWNC--RKKQAGVMLTVG 691
Db 677 TYILLANMLIALMGETVSKIAQESKIWKLQRPITILDIENSYNLCRRSFRSGRRVLVG 736
QY 692 TKPDGSPDERWCFRVEEVNWSWEQTLPTLCEDPSGAG 729
Db 737 ITPDGQDDYRWCFRVDENVNWSWTNLTNLGIINEDPGCSG 774
```

RESULT 9

```
US-09-978-303-25
; Sequence 25, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 843
; TYPE: PRT
; ORGANISM: chicken
US-09-978-303-25
```

```
Query Match 42.2%; Score 1689; DB 4: Length 843;
Best Local Similarity 47.2%; Pred. No. 6.4e-150;
Matches 358; Conservative 118; Mismatches 218; Indels 64; Gaps 12;

QY 4 PSSSPVFRLETLDCGQEDGSEADRGKL---DFGSGLPMPMESQFQGEDRKFAPQ--IRVNIN 59
Db 49 PSKSNIF-----ARRGRFVWGDCDKMAPMDSFYQ--MDHLMAFSVVKFHAN 93
QY 60 YRKQ-----TGASQPDNRPDRDLFNASVGRVPEDLAGLPEYLSKTSKYLTS 108
Db 94 MERGKHLKLLSDTSITGCSKAFKFEYDRRIIFDAVARGSTKDLDDLLLYLNRLKHLTDD 153
QY 109 EYTEGSTGCTCKMLKAVLNKDGYNACILPLLQIQRDSDGNPQPLVNAQCTDDYYRGHSALH 168
Db 154 EFKEPETGKTCLLKAAMLNLDHGKNDITPLLLDIAKKTGTLKEFVNAYETDNYTKGQTALH 213
QY 169 IAIEKRSLOCVKLLVNGANVHARACGRFFQKQG--TCFYFGELPLSLAACTKQMDVWSY 227
Db 214 IAIERENMYLVKLLVQNGADVHARACGEFFRKIKGKPGFYFGELPLSLAACTNQLCIVKF 273
QY 228 LLENPHQASLOATDSQNTVLHALVMSDNSAENIALVTSMDGLLQAGARLCPTVQLE 287
Db 274 LLENPYQAADIAAEDSMGNMVLHTLVEIADNTKNTKFTVMNNILILGAKINPILKLE 333
QY 288 DIRNLQDLTPLKAAKEGKIEFRHILQREFSG--LSHLSRKFTWCYGPVRVSLYDLAS 345
Db 334 ELTNKKGLTPLTAAKTGKIGIPAYILRREIKDPCRHSRKFTWAYGPHVSSLYDLSC 393
QY 346 VDSCEBNSVLEIIAFHCKSPHRRMVVLEPLNKLQAKWDLLIPK--FFLNFLCNLIYMPI 404
Db 394 IDTCEKNSVLEIIAYSSETPNRHEMLLVPEPLNLLQDKWDRFVKHLFYFNFFVYAIHISI 453
QY 405 FTAVAYHOPTLKQAAAPH--LKAEVGNSMLLTGHILILGGIYLLVQGLWYFWRHVFIMI 463
Db 454 LTTAAAYRVPQKDGKPPFAFGHSTGEYFRVTGEILSVLGLYFFFRGIQYFVQRRPSLKT 513
QY 464 SFIDSYPEILFQALLTVVSOVLCLAEIEMVLPPLVLSALVGLMNLVYTRGFOHTGIY 523
Db 514 LIVDSYSEVLFVHSLLSVVLYFCQGLYVASMVFSALGWMANMLYTRGFOOMGIY 573
QY 524 SVMIOKVILRLRFLLIYLVFLGFAVALVSLSQEAWRPEAPTGNATESVQPMEGQBD 583
Db 574 SVMIAKMILRDLRCRFMFVLYVFLGFASTAVTLIED-----DNEGQDT 616
QY 584 EGN-----GAQYRGILEASLELFKFTTGMGELAFQBLHPRGMVLLLLAYVLL 632
Db 617 NSSEYARCSHTRKGRTSYNSLYYTCLLEFKFTTGMGDLFTENYRFSKVFLVLLVYL 676
QY 633 TYILLANMLIALMSETVNSVATDSIWKLOKAIISVLEMENGYWNC--RKKQAGVMLTVG 691
Db 677 TYILLANMLIALMGETVSKIAQESKIWKLQRPITILDIENSYNLCRRSFRSGRRVLVG 736
QY 692 TKPDGSPDERWCFRVEEVNWSWEQTLPTLCEDPSGAG 729
Db 737 ITPDGQDDYRWCFRVDENVNWSWTNLTNLGIINEDPGCSG 774
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RESULT 10

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US-09-235-451-2
; Sequence 2, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
```

;
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 838
; TYPE: PRT
; ORGANISM: R. rattus
US-09-235-451-2

Query Match 41.3%; Score 1652; DB 3; Length 838;
Best Local Similarity 46.3%; Pred. No. 1.9e-146;
Matches 359; Conservative 127; Mismatches 230; Indels 60; Gaps 15;
QY 18 GQDGEADRGKLDGSGGLPPMESQFQEDRKFAPOIRVN---LNYRKGTG----- 65
DB 51 GKGDSEAS-----PLDCPYEEGGLASCPITVSSVLTIQRPDGPASVRPSSQ 99
QY 66 ----ASQPDNPRDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTSEYTEGSGTKTCLM 121
DB 100 DSVSAGEKPPRLYDRRSIFDAVAQNCQELSLPLFLQSKKRLTDSFKDPETGKTCLL 159
QY 122 KAVLNKDGVNACILPLQIDRDSGNPQPLVNAQCTDDYVRGHSALHIAIEKRSLOCVKL 181
DB 160 KAMNLNHNQNDTIALLDVARKTSLKQFVNASYTDSYKGTALHIAIERNNMTLVL 219
QY 182 LVENGANVHARACGRPFQKQGG--TCFYFGEPLPLSLAACTQMDVSVSYLLENPHQPASLOA 240
DB 220 LVENGADVQAANGDFPKTKGPGFYFGEPLPLSLAACTNQLAIVKFLQNSQPADISA 279
QY 241 TDSQGNVTLHALVMSIDNSAENIALVTSYDGLLOAGARLCPTVQLIEDIRNLDLPLKL 300
DB 280 RDSVGNVTLHALVEADVNTVDNTKFTVSMYNEILILGAKLHPTLKLEETNRKGLTPLAL 339
QY 301 AAKEGKTEIHRHILQREF--SGLSHLSRKTEWCYGPVRVSLYDLASVDSCEANSVLEII 358
DB 340 AASSGKIGVLAYILQREIHEPECRHLSRKTEWAYGPHVSHSLYDLSCIDTCEKNSVLEVI 399
QY 359 AP-HCKSPHRRMVLEPLNKLQAKWDLIPK--FFLNFLCNLIYMFIFTAAYHQPITLK 416
DB 400 AYSSETPNRHDMLLVEPLNRLQDKWDRFVKRIFNFYFVCLYMIIFTAAAYRPV-- 457
QY 417 KQAAP--HLKAEVGNMMLTGHILILGGLIYLLVQGLWYFWRHVFIIWISFIDSYBILF 474
DB 458 -EGLPPYKLNVTGDIYFRVTGEILSVSGGVYFFRGIQYFLQRRPSLSLFDVDSYBILF 516
QY 475 LFQALLTVVSQVLCFLAEIWEYLPLLVSAVLGMLNLLYYTRGQHTGIYSVMIOKVILRD 534
DB 517 FVQSLFMLSVLVYFSQRKEYVASWVFLAMGWTNMLYYTRGQQMGIVAVMIKMLIRD 576
QY 535 LLRFLLIYVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEGDEGNGA----- 588
DB 577 LCRFMFVYLVFLFGFSTAVVTLLIED-----GKN---NSLPWESTPHKCRSACKPGN 625
QY 589 QYRGILEASLELPKFTIGMGLAFQELHFRGMVLLLLAYVLLTYTILLNMLIALMSET 648
DB 626 SYNLSYTCLELFPKFTIGMGLDLETENYDKAVFIILLAYVILTYTILLNMLIALMGET 685
QY 649 VNSVATDSWSIWKLOKAIISVLEMBNGYWC--RKKQAGVMLTVGTGPDGSPDRCWRPVE 707
DB 686 VNKIAQESKNWKLOQRAITILDTKESFLKCMKRAFRSGKLLQVGTTPDGKDDYRWCPRVD 745
QY 708 EVNWASWEQTLPTLCEDPSGA-GVPRILENPVLASPPKEDEBGASEENYVPVOLLIQ 762
DB 746 EVNWTNTNVTNVIINEDPGNCEGVKRTLSFSLRSG-----RVSGRNWKNFALVPLLR 797

RESULT 11

US-09-132-316-3
; Sequence 3, Application US/09132316B
; Patent No. 644440
; GENERAL INFORMATION:
; APPLICANT: Young, Paul E.
; APPLICANT: Ruben, Steven M.

;
; TITLE OF INVENTION: Vanilloid Receptor-2
; FILE REFERENCE: 1488.1110000
; CURRENT APPLICATION NUMBER: US/09/132,316B
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: US 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-132-316-3
Query Match 41.3%; Score 1652; DB 4; Length 838;
Best Local Similarity 46.3%; Pred. No. 1.9e-146;
Matches 359; Conservative 127; Mismatches 230; Indels 60; Gaps 15;
QY 18 GQDGEADRGKLDGSGGLPPMESQFQEDRKFAPOIRVN---LNYRKGTG----- 65
DB 51 GKGDSEAS-----PLDCPYEEGGLASCPITVSSVLTIQRPDGPASVRPSSQ 99
QY 66 ----ASQPDNPRDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTSEYTEGSGTKTCLM 121
DB 100 DSVSAGEKPPRLYDRRSIFDAVAQNCQELSLPLFLQSKKRLTDSFKDPETGKTCLL 159
QY 122 KAVLNKDGVNACILPLQIDRDSGNPQPLVNAQCTDDYVRGHSALHIAIEKRSLOCVKL 181
DB 160 KAMNLNHNQNDTIALLDVARKTSLKQFVNASYTDSYKGTALHIAIERNNMTLVL 219
QY 182 LVENGANVHARACGRPFQKQGG--TCFYFGEPLPLSLAACTQMDVSVSYLLENPHQPASLOA 240
DB 220 LVENGADVQAANGDFPKTKGPGFYFGEPLPLSLAACTNQLAIVKFLQNSQPADISA 279
QY 241 TDSQGNVTLHALVMSIDNSAENIALVTSYDGLLOAGARLCPTVQLIEDIRNLDLPLKL 300
DB 280 RDSVGNVTLHALVEADVNTVDNTKFTVSMYNEILILGAKLHPTLKLEETNRKGLTPLAL 339
QY 301 AAKEGKTEIHRHILQREF--SGLSHLSRKTEWCYGPVRVSLYDLASVDSCEANSVLEII 358
DB 340 AASSGKIGVLAYILQREIHEPECRHLSRKTEWAYGPHVSHSLYDLSCIDTCEKNSVLEVI 399
QY 359 AP-HCKSPHRRMVLEPLNKLQAKWDLIPK--FFLNFLCNLIYMFIFTAAYHQPITLK 416
DB 400 AYSSETPNRHDMLLVEPLNRLQDKWDRFVKRIFNFYFVCLYMIIFTAAAYRPV-- 457
QY 417 KQAAP--HLKAEVGNMMLTGHILILGGLIYLLVQGLWYFWRHVFIIWISFIDSYBILF 474
DB 458 -EGLPPYKLNVTGDIYFRVTGEILSVSGGVYFFRGIQYFLQRRPSLSLFDVDSYBILF 516
QY 475 LFQALLTVVSQVLCFLAEIWEYLPLLVSAVLGMLNLLYYTRGQHTGIYSVMIOKVILRD 534
DB 517 FVQSLFMLSVLVYFSQRKEYVASWVFLAMGWTNMLYYTRGQQMGIVAVMIKMLIRD 576
QY 535 LLRFLLIYVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEGDEGNGA----- 588
DB 577 LCRFMFVYLVFLFGFSTAVVTLLIED-----GKN---NSLPWESTPHKCRSACKPGN 625
QY 589 QYRGILEASLELPKFTIGMGLAFQELHFRGMVLLLLAYVLLTYTILLNMLIALMSET 648
DB 626 SYNLSYTCLELFPKFTIGMGLDLETENYDKAVFIILLAYVILTYTILLNMLIALMGET 685
QY 649 VNSVATDSWSIWKLOKAIISVLEMBNGYWC--RKKQAGVMLTVGTGPDGSPDRCWRPVE 707
DB 686 VNKIAQESKNWKLOQRAITILDTKESFLKCMKRAFRSGKLLQVGTTPDGKDDYRWCPRVD 745
QY 708 EVNWASWEQTLPTLCEDPSGA-GVPRILENPVLASPPKEDEBGASEENYVPVOLLIQ 762
DB 746 EVNWTNTNVTNVIINEDPGNCEGVKRTLSFSLRSG-----RVSGRNWKNFALVPLLR 797

RESULT 12

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US-09-667-422-9
; Sequence 9, Application US/09667422
; Patent No. 6482611
; GENERAL INFORMATION:
; APPLICANT: Cortright, Daniel
; APPLICANT: Krause, James
; TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
; FILE REFERENCE: HCR
; CURRENT APPLICATION NUMBER: US/09/667,422
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Rattus sp.
; PUBLICATION INFORMATION:
; AUTHORS: Caterina, Michael J.
; AUTHORS: Schumacher, Mark A.
; AUTHORS: Tominaga, Makoto
; AUTHORS: Rosen, Tobias A.
; TITLE: The capsaicin receptor: a heat-activated ion channel in
; TITLE: the pain pathway
; JOURNAL: Nature
; VOLUME: 389
; PAGES: 816-824
; DATE: 1997
; US-09-667-422-9

Query Match 41.3%; Score 1652; DB 4; Length 838;
Best Local Similarity 46.3%; Pred. No. 1.9e-146;
Matches 359; Conservative 127; Mismatches 230; Indels 60; Gaps 15;

QY 18 GOEDGSEADRGKLDGSGLPMMESQFQGEDRKFAPQIRVN---LNYRKGTG----- 65
DB 51 GKGDSEAS-----PLDCPYEGGLASCPIITVSSVLTIQRPDGPASVPPSQ 99

QY 66 ----ASQPDPNRDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCLM 121
DB 100 DSVSAGEKPPRLYDRRSIFDVAQNCQELSLPLFLQSKKRLTDSEFKDPETGKTCLL 159

QY 122 KAVLNKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYRGHSAHIAIEKRSLOCVKL 181
DB 160 KAMLNHNGQNDTIALLLDVARKTDSLQKQFVNASYTDYSGQTALHIAIERNNMTLVLT 219

QY 182 LVENGANVHARACGRFFQKQOG--TCFYFGEPLPLSLAACTKQMDVSVYLLNPHOPASLOA 240
DB 220 LVENGADVQAANGDFFKTKGRPGFYFGEPLPLSLAACTNQLAIVKFLQNSWQPADISA 279

QY 241 TDSQGNTVLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPVTQVLEDIRNLQDLPKL 300
DB 280 RDSVGNVTLHALVEVADNTVDNTKFTVSMYNEILILGAKLHPTLKLEBITNRKGLTPLAL 339

QY 301 AAKEGKIEIFRHILQREF--SGLSHLRKFTEWCYGPVRVSLYDLASVDSCEANSVLEII 358
DB 340 AASSGKIGVLAYILOREIHEPECRHLRKRFTBWAQPVHSSLYDLSCIDTCENSVLEVI 399

QY 359 AF-HCKSPHRRMVVLEPLNKLQAKWDLILPK-FFLNPLCNLIYMFIFTAAYHOPTLK 416
DB 400 AYSSSETPNRHMVLEPLNKLQAKWDRFVKRIFVFNFFVYCLYMIIFTAAAYRPV-- 457

QY 417 KQAAP--HLKAEVGNMGLTHGILLGGIYLLAVGQWYFRRHVFIFWISFIDSYEILF 474
DB 458 -EGLPPVKLNTVDYFRVTGELSVSGGVYFFRGIQYFLQRPSSLKSLFVDSYSEILF 516

QY 475 LFOALLTVVSQVLCFLAIEWYLPVLSALVGLHNLNLYYTRGQHTGYISVMLOKVIIRD 534
DB 517 FVQSLFMLVSWLYFSQKEYVNASVFLAMGTNNMLYTRGQQMGIVAVMIERKILRD 576

QY 535 LIRFLIYLVFLFGFAVALVLSQEAWRPEAPTPGNATESVQPMQGOEBGNGA----- 588
DB 577 LCRFMFVYLVFLGFGFAVTVLLIED-----GKN---NSLPWESTPHKCRGSACKPGN 625

US-09-978-303-2
; Sequence 2, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 838
; TYPE: PRT
; ORGANISM: R. rattus
; US-09-978-303-2

Query Match 41.3%; Score 1652; DB 4; Length 838;
Best Local Similarity 46.3%; Pred. No. 1.9e-146;
Matches 359; Conservative 127; Mismatches 230; Indels 60; Gaps 15;

QY 18 GOEDGSEADRGKLDGSGLPMMESQFQGEDRKFAPQIRVN---LNYRKGTG----- 65
DB 51 GKGDSEAS-----PLDCPYEGGLASCPIITVSSVLTIQRPDGPASVPPSQ 99

QY 66 ----ASQPDPNRDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCLM 121
DB 100 DSVSAGEKPPRLYDRRSIFDVAQNCQELSLPLFLQSKKRLTDSEFKDPETGKTCLL 159

QY 122 KAVLNKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYRGHSAHIAIEKRSLOCVKL 181
DB 160 KAMLNHNGQNDTIALLLDVARKTDSLQKQFVNASYTDYSGQTALHIAIERNNMTLVLT 219

QY 182 LVENGANVHARACGRFFQKQOG--TCFYFGEPLPLSLAACTKQMDVSVYLLNPHOPASLOA 240
DB 220 LVENGADVQAANGDFFKTKGRPGFYFGEPLPLSLAACTNQLAIVKFLQNSWQPADISA 279

QY 241 TDSQGNTVLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPVTQVLEDIRNLQDLPKL 300
DB 280 RDSVGNVTLHALVEVADNTVDNTKFTVSMYNEILILGAKLHPTLKLEBITNRKGLTPLAL 339

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QY 359 AF-HCKSPHRRMVVLEPLNKLQAKWDLILPK-FFLNPLCNLIYMFIFTAAYHOPTLK 416
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QY 417 KOAAP--HLKAEYGNMMLTGHILILGGIYLLVGLQWYFWRRHVFIMWISFIDSYEILF 474
DB 458 -EGLPYKLNKNTVGDYFVRTGTEILSVGGYFFFRGIQYFLQRRPSLKSILFVDSYSEILF 516
QY 475 LFOALTVVSQVLCFLAIEWYLLPLVLSALVGLWNLVYTRGPHQHTGIYSVMIQVILRD 534
DB 517 FVQSLFMLSVALVYFSQRKEYVASMVFSLANGMTNMLYTRGQQMGYIYAVMIERKILRD 576
QY 535 LLRFLIYLVFLRFGFAVALVLSQEAWRPEAPTPGNATESVQPMQOEDEGNA----- 588
DB 577 LCRFMFVYLVFLRFGFAVVTLLIED-----GKN---NSLPWESTPHKCRGSACKPGN 625
QY 589 QYRGILEASLELKFPTIGMELAFQEOQLHFRGMVLLLLAYVLLTYLLINMLIALMSET 648
DB 626 SYNSLVSCTCLELKFPTIGMDLEFTENYDFKAVFIILLAYVILTYLLINMLIALMGET 685
QY 649 VNSVATDSMSIWLKQAKAISVLEMGYWC-RKKORAGVMLTVGTGPDGSPDRWCFRVE 707
DB 686 VNKIAQESKNWKLQRAITILDTEKSPKCMKRAFRSGKLLQVFTPDGKDDYRWCPRVD 745
QY 708 EVNWASHEQTLPTLCEDPSGA-GVPRITLENPVLASPPKEDGASBENTYVPVOLLQ 762
DB 746 EVNWTTNVTNGIINEDPGNCEGVKRTLSFSLRSG-----RVSGRNKNFALVPLLR 797

RESULT 14

US-09-667-422-4
; Sequence 4, Application US/09667422
; Patent No. 6482611
; GENERAL INFORMATION:
; APPLICANT: Cortright, Daniel
; APPLICANT: Krause, James
; TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
; FILE REFERENCE: HCR
; CURRENT APPLICATION NUMBER: US/09/667,422
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (434)..(455)
; OTHER INFORMATION: TM1
; NAME/KEY: TRANSMEM
; LOCATION: (480)..(495)
; OTHER INFORMATION: TM2
; NAME/KEY: TRANSMEM
; LOCATION: (510)..(530)
; OTHER INFORMATION: TM3
; NAME/KEY: TRANSMEM
; LOCATION: (543)..(569)
; OTHER INFORMATION: TM4
; NAME/KEY: TRANSMEM
; LOCATION: (577)..(596)
; OTHER INFORMATION: TM5
; NAME/KEY: TRANSMEM
; LOCATION: (656)..(684)
; OTHER INFORMATION: TM6
US-09-667-422-4

Query Match 41.2%; Score 1651.5; DB 4; Length 839;
Best Local Similarity 48.5%; Pred. No. 2.2e-146;
Matches 344; Conservative 122; Mismatches 199; Indels 45; Gaps 11;

QY 74 FDRDLFNASRGVPELAGLPEYLSKTSKYLTDSBYETGSKTCLMKAVNLKDGVA 133
DB 113 YDRSIFEAQNQCQDLSELLLQKSKHGLTDFNEFKDPETGKTCLLKAMLNLDGNT 172
QY 134 CILPLQLIDRDSGNPQPLVNAQCTDDYYRGHSALHIAEKRSQCCKLLVNGANVHARA 193

DB 173 TIPLLEIARQTDSEKELVNASYTDSSYKQGTALHIAIBERRNMAVLTLLVENGADVQAAA 232
QY 194 CORFFQKQG--TCFYFGEPLPLSLAACTTQOWDVVSVLLENPHOPASLOAQDSQONTVLHAL 252
DB 233 HDGFPAKTKGRGPFYFGEPLPLSLAACTNQLGIVKVELLQNSWTADISARDSVGNVTLHAL 292
QY 253 VMISDASBNIALVTSMDGLLOAGARLCTVOLEDIRNLQDLTPUKLAAGKGGKIBIFRH 312
DB 293 VEADVNTADNTKFTVSMYNEILMLGAKLHPTLKLBELTNKKGMTPLALAAAGTGKIGVLA 352
QY 313 ILORFES--GLSHLSRKFTWCYGPVRSVLYDLASVDSCEENSVLRIIAF-HCKSPHRHR 369
DB 353 ILQRIQBEPCRHLSRKFTWYAGPVHSSLYDLSCIDTCEKNSVLBIAYSSSETPNRHD 412
QY 370 MVVLEPLNKLQAKQDILLIPK--FFLNFLCNLYMFIETAVAYHQPRTLKQAAAPHLKAE-V 427
DB 413 MLIVLEPLNELLQDKWDRFVKRIFYFNFLVYCLYMIIFTWAAYYRPV---DGLPPFKMEKI 469
QY 428 GNSMLLTGHILILGGIYLLVGLQWYFWRRHVFIMWISFIDSYEILFLOALTVVSQVL 487
DB 470 GDYFRTVBILSVLGGVYFFFRGIQYFLQRRPSMKTFLVDSYSEMLFFLQSLFMLATVVL 529
QY 488 CFLATEWYLLPLVLSALVGLWNLVYTRGFOHTGIYSVMIQVILRDLLRFLIYLVFLF 547
DB 530 YFSLHKEYVASMVFSALGNTNMLYTRGFOQGIYAVMIERKMILRDLCRFMFYIYVFLF 589
QY 548 GFAVALVLSQEA-----WRPEAPTPGNATESVQPMQOEDEGNGAQYRGIL 594
DB 590 GFSTAVVLLIEDKNDLSLSESTSHRWGPACPPDSS-----YNSLY 632
QY 595 EASLELFKFTIGMELAFQEOQLHFRGMVLLLLAYVLLTYLLINMLIALMSETVNSVAT 654
DB 633 STCLELFKFTIGMDLEFTENYDFKAVFIILLAYVILTYLLINMLIALMSETVNSVAT 692
QY 655 DWSIWLKQAKAISVLEMGYWC-RKKORAGVMLTVGTGPDGSPDRWCFRVEENVAS 713
DB 693 ESKNIWLQRAITILDTEKSPKCMKRAFRSGKLLQVGYTPDGKDDYRWCFRVDEVNMTT 752
QY 714 WEQTLPTLCEDPSGA-GVPRITLENPVLASPPKEDGASBENTYVPVOLLQ 762
DB 753 WNTNVTNGIINEDPGNCEGVKRTLSFSLRSG-----RVSGRNKNFALVPLLR 798

RESULT 15

US-09-197-636-2
; Sequence 2, Application US/09197636
; Patent No. 6239267
; GENERAL INFORMATION:
; APPLICANT: DUCKWORTH, DAVID
; APPLICANT: HAYES, PHILIP
; APPLICANT: MEADOWS, HELEN
; APPLICANT: DAVIS, JOHN
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US
; ZIP: 19482-0980
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,636
; FILING DATE: 23-NOV-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 9805137.8

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QM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:51:46 ; Search time 1573 Seconds
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Title: US-09-445-614B-1

Perfect score: 2469

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Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA:*

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26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2462.2	99.7	2809	24	US-11-013-090-4
3	2455.8	99.5	2825	16	US-10-168-651-30
4	2447.4	99.1	2867	17	US-10-264-237-1401
5	2424.6	98.2	2805	14	US-10-137-316-1
6	2378.4	96.3	2380	10	US-09-978-303-35
7	2378.4	96.3	2380	21	US-10-915-017-35

8	2293.4	92.9	2295	17	US-10-342-844-67	Sequence 67, Appl
9	2292	92.8	2292	24	US-11-013-090-6	Sequence 6, Appl
10	2263.2	91.7	2295	17	US-10-342-844-69	Sequence 69, Appl
11	2259.2	91.5	2279	10	US-09-809-391-191	Sequence 191, Appl
12	2259.2	91.5	2279	10	US-09-882-171-191	Sequence 191, Appl
13	2259.2	91.5	2279	17	US-10-164-861-191	Sequence 191, Appl
14	2061.8	83.5	2860	10	US-09-809-391-314	Sequence 314, Appl
15	2061.8	83.5	2860	10	US-09-882-171-314	Sequence 314, Appl
16	2061.8	83.5	2860	17	US-10-164-861-314	Sequence 314, Appl
17	1933.4	78.3	1935	17	US-10-342-844-43	Sequence 43, Appl
18	1572	63.7	2824	21	US-10-764-420-2281	Sequence 2281, Appl
19	1535.8	62.2	2271	17	US-10-342-844-51	Sequence 51, Appl
20	1529.4	61.9	2271	17	US-10-342-844-85	Sequence 85, Appl
21	1522.4	61.7	2736	10	US-09-978-303-3	Sequence 3, Appl
22	1522.4	61.7	2736	21	US-10-915-017-3	Sequence 3, Appl
23	1459.6	59.1	2286	17	US-10-342-844-45	Sequence 45, Appl
24	1458	59.1	2286	17	US-10-342-844-33	Sequence 33, Appl
25	1445.6	58.6	2289	17	US-10-342-844-97	Sequence 97, Appl
26	1098.4	44.5	1794	24	US-11-013-090-10	Sequence 10, Appl
27	1065.8	43.2	1662	24	US-11-013-090-12	Sequence 12, Appl
28	1007.4	40.8	1489	24	US-11-013-090-7	Sequence 7, Appl
29	1005.4	40.7	1308	24	US-11-013-090-9	Sequence 9, Appl
30	750.8	30.4	884	10	US-09-978-303-22	Sequence 22, Appl
31	750.8	30.4	884	21	US-10-915-017-22	Sequence 22, Appl
32	711	28.8	876	10	US-09-809-391-315	Sequence 315, Appl
33	711	28.8	876	10	US-09-882-171-315	Sequence 315, Appl
34	711	28.8	876	17	US-10-164-861-315	Sequence 315, Appl
35	675.4	27.4	891	21	US-10-479-081-7	Sequence 7, Appl
36	662.4	26.8	2517	24	US-11-013-090-3	Sequence 3, Appl
37	662.4	26.8	2520	17	US-10-342-844-47	Sequence 47, Appl
38	662.4	26.8	2520	17	US-10-342-844-73	Sequence 73, Appl
39	662.4	26.8	2520	17	US-10-342-844-81	Sequence 81, Appl
40	662.4	26.8	3261	17	US-10-191-997-120	Sequence 120, Appl
41	662.4	26.8	3909	24	US-11-013-090-1	Sequence 1, Appl
42	662.4	26.8	4182	14	US-10-246-435-2	Sequence 2, Appl
43	662.4	26.8	4203	14	US-10-246-435-1	Sequence 1, Appl
44	660.8	26.8	2520	17	US-10-342-844-41	Sequence 41, Appl
45	660.8	26.8	2544	10	US-09-978-303-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-10-757-262-25
; Sequence 25, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32220, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; TITLE OF INVENTION: 55053
; FILE REFERENCE: MPI03-007P1RNMNMIM
; CURRENT APPLICATION NUMBER: US/10757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614


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/ PRIOR FILING DATE: 2003-05-19
/ PRIOR APPLICATION NUMBER: US 60/478,742
/ PRIOR FILING DATE: 2003-06-16
/ PRIOR APPLICATION NUMBER: US 60/488,529
/ PRIOR FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: US 60/491,156
/ PRIOR FILING DATE: 2003-07-30
/ PRIOR APPLICATION NUMBER: US 60/499,594
/ PRIOR FILING DATE: 2003-09-02
/ PRIOR APPLICATION NUMBER: US 60/506,332
/ PRIOR FILING DATE: 2003-09-26
/ NUMBER OF SEQ ID NOS: 136
/ SOFTWARE: PastSeq for Windows Version 4.0
/ SEQ ID NO 25
/ LENGTH: 2809
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (361)...(2655)
/ US-10-757-262-25

Query Match          99.7%; Score 2462.2; DB 19; Length 2809;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2464; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3  CGAGGCGGACGCGCAGCTGGGAGGAAAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG 62
DB      |
DB      267 CAACACCGACGCGCAGCTGGGAGGAAAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG 326
QY      |
QY      63  TCTTGCTGACCGAGCAGCCTCTCTCTAGATGACCTCACCCCTCCAGCTCTCCAGT 122
DB      |
DB      327 TCTTGCTGACCGAGCAGCCTCTCTCTAGATGACCTCACCCCTCCAGCTCTCCAGT 386
QY      |
QY      123 TTTTCAGGTTGGAGACATTAGATGAGGCGCAAGAGATGGCTCTGAGGCGGACAGAGGAAA 182
DB      |
DB      387 TTTTCAGGTTGGAGACATTAGATGAGGCGCAAGAGATGGCTCTGAGGCGGACAGAGGAAA 446
QY      |
QY      183 GCTGGAATTTGGAGCGGGTGCTCCATGAGAGTCAAGTTCACGGGCGAGGACCGGAA 242
DB      |
DB      447 GCTGGAATTTGGAGCGGGTGCTCCATGAGAGTCAAGTTCACGGGCGAGGACCGGAA 506
QY      |
QY      243 ATTGCGCCCTCAGATAAGTCAACTCACTACCGAAGGAAACAGGTGCGAGTCAGCC 302
DB      |
DB      507 ATTGCGCCCTCAGATAAGTCAACTCACTACCGAAGGAAACAGGTGCGAGTCAGCC 566
QY      |
QY      303 GGAATCCAAACCGAATTTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCGCCGA 362
DB      |
DB      567 GGAATCCAAACCGAATTTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCGCCGA 626
QY      |
QY      363 GGAATCTGGCTGGAATTTCCAGAGTACCTGAGCAAGACAGCAAGTACTCAACGACTCGGA 422
DB      |
DB      627 GGAATCTGGCTGGAATTTCCAGAGTACCTGAGCAAGACAGCAAGTACTCAACGACTCGGA 686
QY      |
QY      423 ATACACAGAGGGCTCCACAGGTAAAGCTGCTGATGAGGCTGTGCTGAACCTTAAGGA 482
DB      |
DB      687 ATACACAGAGGGCTCCACAGGTAAAGCTGCTGATGAGGCTGTGCTGAACCTTAAGGA 746
QY      |
QY      483 CGGAGTCAATGCTGCAATTTGCGCACTGCTGCAGATCGACAGGAGCTCTGGCAATCTCTCA 542
DB      |
DB      747 CGGAGTCAATGCTGCAATTTGCGCACTGCTGCAGATCGACAGGAGCTCTGGCAATCTCTCA 806
QY      |
QY      543 GCCCCTGGTAAATGCCAGTGCGACAGATGACTATTACCGAGGCGCACAGCGCTCTGCACAT 602
DB      |
DB      807 GCCCCTGGTAAATGCCAGTGCGACAGATGACTATTACCGAGGCGCACAGCGCTCTGCACAT 866
QY      |
QY      603 CGCCATTGAGAGAGGAGTCTGCGATGTGTGAAGCTCTCGTGAGGAATGGGGCCCAATGT 662
DB      |
DB      867 CGCCATTGAGAGAGGAGTCTGCGATGTGTGAAGCTCTCGTGAGGAATGGGGCCCAATGT 926
QY      |
QY      663 GCATGCCCGGGCTGCGGGCGCTTCTTCCAGAGGGGCGCAAGGAGCTTGTCTTTTATTTCCG 722
DB      |
DB      927 GCATGCCCGGGCTGCGGGCGCTTCTTCCAGAGGGGCGCAAGGAGCTTGTCTTTTATTTCCG 986
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QY      723 TGAGCTACCCCTCTCTTTGGCGGCTTGACACAGCAGTGGGATGTGGTAAGCTACCTCTCT 782
DB      |
DB      987 TGAGCTACCCCTCTCTTTGGCGGCTTGACACAGCAGTGGGATGTGGTAAGCTACCTCTCT 1046
QY      |
QY      783 GGAGAAACCCACACACAGCGCGCAGCTGCAGGCGCACTGACTCCAGGGGCAACACAGTCTCT 842
DB      |
DB      1047 GGAGAAACCCACACACAGCGCGCAGCTGCAGGCGCACTGACTCCAGGGGCAACACAGTCTCT 1106
QY      |
QY      843 GCATGCCCTAGTGTGATCTCGGACAACTCAGCTGAGAACTGTCATCTGTCAGCAGCAT 902
DB      |
DB      1107 GCATGCCCTAGTGTGATCTCGGACAACTCAGCTGAGAACTGTCATCTGTCAGCAGCAT 1166
QY      |
QY      903 GTATGATGGGCTCTCTCAAGCTGGGCGCGCTCTGCCCTTCCCTGACCTTGTAGGACAT 962
DB      |
DB      1167 GTATGATGGGCTCTCTCAAGCTGGGCGCGCTCTGCCCTTCCCTGACCTTGTAGGACAT 1226
QY      |
QY      963 CGCAACCTGACAGGATCTCACGCTCTGAAAGCTGGCGCGCAAGAGGGGCAAGATCGAGAT 1022
DB      |
DB      1227 CGCAACCTGACAGGATCTCACGCTCTGAAAGCTGGCGCGCAAGAGGGGCAAGATCGAGAT 1286
QY      |
QY      1023 TTTTCAGGACATCTGACAGCGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTTCA 1082
DB      |
DB      1287 TTTTCAGGACATCTGACAGCGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTTCA 1346
QY      |
QY      1083 CGAGTGGTGTATGGGCTGTCCGGGTGTCGCTGTATGACCTGGCTTCTGTGACAGCTG 1142
DB      |
DB      1347 CGAGTGGTGTATGGGCTGTCCGGGTGTCGCTGTATGACCTGGCTTCTGTGACAGCTG 1406
QY      |
QY      1143 TGAGAGAACTCAGTGTCTGAGATCATTTGCCCTTTTCAATGCAAGAGCCCGCACCGAC 1202
DB      |
DB      1407 TGAGAGAACTCAGTGTCTGAGATCATTTGCCCTTTTCAATGCAAGAGCCCGCACCGAC 1466
QY      |
QY      1203 AATGTCGTTTTGGAGCCCTGAAACAACTGTGACAGGCGAAATGGGATCTGCTCATCCC 1262
DB      |
DB      1467 AATGTCGTTTTGGAGCCCTGAAACAACTGTGACAGGCGAAATGGGATCTGCTCATCCC 1526
QY      |
QY      1263 CAAGTTCCTTTAAACTTCTGTGTAATCTGATCTACATGTTTCATCTTCCCGCTGTGC 1322
DB      |
DB      1527 CAAGTTCCTTTAAACTTCTGTGTAATCTGATCTACATGTTTCATCTTCCCGCTGTGC 1586
QY      |
QY      1323 CTACCATCAGCTTACCTGAAAGCAGGCGCGCCCTCACCTGAAAGCGGAGTTGGAAA 1382
DB      |
DB      1587 CTACCATCAGCTTACCTGAAAGCAGGCGCGCCCTCACCTGAAAGCGGAGTTGGAAA 1646
QY      |
QY      1383 CTCCATGCTGTGAAGGGGCAATCTCTTATCTGTGAGGGGGAATCTAATCTCTCTGTTGG 1442
DB      |
DB      1647 CTCCATGCTGTGAAGGGGCAATCTCTTATCTGTGAGGGGGAATCTAATCTCTCTGTTGG 1706
QY      |
QY      1443 CCAGCTGTGGTACTTCTGGGCGGCGCACTGTTTCATCTCGATCTCGTTCATAGACAGCTA 1502
DB      |
DB      1707 CCAGCTGTGGTACTTCTGGGCGGCGCACTGTTTCATCTCGATCTCGTTCATAGACAGCTA 1766
QY      |
QY      1503 CTTTGAATTCCTTCTCTGTTCCAGGCGCTGCTCAAGTGTGTCTCCAGGTGTGTGTTT 1562
DB      |
DB      1767 CTTTGAATTCCTTCTCTGTTCCAGGCGCTGCTCAAGTGTGTCTCCAGGTGTGTGTTT 1826
QY      |
QY      1563 CTTGGCCATCGAGTGTGTACTTGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1622
DB      |
DB      1827 CTTGGCCATCGAGTGTGTACTTGCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1886
QY      |
QY      1623 CTTGCTTTTACTATACAGTGGCTTCCAGCACACAGGACTCTACAGTGTCTATGATCCAGAA 1682
DB      |
DB      1887 CTTGCTTTTACTATACAGTGGCTTCCAGCACACAGGACTCTACAGTGTCTATGATCCAGAA 1946
QY      |
QY      1683 GGTTCATCTCGGGGACTCTGCGCTTCTCTTCTGATCTACTTAGTCTTCTTTTCGGCTT 1742
DB      |
DB      1947 GGTTCATCTCGGGGACTCTGCGCTTCTCTTCTGATCTACTTAGTCTTCTTTTCGGCTT 2006
QY      |
QY      1743 CGCTGTAGCCCTGGTGAGCCTTGAGCCAGGAGCTTGGCGCGCCCGAAAGCTCTCTACAGGCC 1802
DB      |
DB      2007 CGCTGTAGCCCTGGTGAGCCTTGAGCCAGGAGCTTGGCGCGCCCGAAAGCTCTCTACAGGCC 2066
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; OTHER INFORMATION: Incyte ID No. US20030171275A1 2446438CB1
US-10-168-651-30

Query Match		99.5%;	Score 2455.8;	DB 16;	Length 2825;
Best Local Similarity		99.7%;	Pred. No. 0;		
Matches 2460;		Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
QY	3	CGAGGCGGACGCGCAGCTGGAGGAAAGACAGGACCTTGACATCTCCATCTGCACAGAGG	62		
DB	318	CAACACGACCGCCAGCTGGAGGAAAGACAGGACCTTGACATCTCCATCTGCACAGAGG	377		
QY	63	TCCTGGCTGGACCGAGCAGCTCTCTCTCTAGGATGAACCTCAACCTCCAGCTCTCCAGT	122		
DB	378	TCCTGGCTGGACCGAGCAGCTCTCTCTCTAGGATGAACCTCAACCTCCAGCTCTCCAGT	437		
QY	123	TTTCAGGTTGGAGACATTAGATGGAGCCCAAGAGATGGCTCTGAGCGCGACAGAGAAA	182		
DB	438	TTTCAGGTTGGAGACATTAGATGGAGCCCAAGAGATGGCTCTGAGCGCGACAGAGAAA	497		
QY	183	GCTGGATTTTGGAGCGGGCTGCTCCCATGGAGTCAAGTTCACGGCGGAGACCGGAA	242		
DB	498	GCTGGATTTTGGAGCGGGCTGCTCCCATGGAGTCAAGTTCACGGCGGAGACCGGAA	557		
QY	243	ATTGCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAAGGAAACAGGTGCCAGTCAGCC	302		
DB	558	ATTGCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAAGGAAACAGGTGCCAGTCAGCC	617		
QY	303	GGATCCAAACCGATTTGACGAGATCGGCTCTTCAATCGGCTCTCCGGGGGTGTCGCCGA	362		
DB	618	GGATCCAAACCGATTTGACGAGATCGGCTCTTCAATCGGCTCTCCGGGGGTGTCGCCGA	677		
QY	363	GGATCTGGCTGGACTTCCAGAGTACCTGACAGACCCAGCAAGTACCTCAACCGACTCGGA	422		
DB	678	GGATCTGGCTGGACTTCCAGAGTACCTGACAGACCCAGCAAGTACCTCAACCGACTCGGA	737		
QY	423	ATACACAGAGGGCTCCAAGGTAAGAGTGCCTGATGAAGGCTGTGTGAACCTTAAGGA	482		
DB	738	ATACACAGAGGGCTCCAAGGTAAGAGTGCCTGATGAAGGCTGTGTGAACCTTAAGGA	797		
QY	483	CGAGTCAATGCTGCAATCTGCGCATCTGCGATGCGAGGACCTGCGCAATCTCTCA	542		
DB	798	CGGGGTCAATGCTGCAATCTGCGCATCTGCGATGCGAGGACCTGCGCAATCTCTCA	857		
QY	543	GCCCTGGTAAATGCCAGTGCAAGATGACTATACCGAGGCGCACAGCGCTCTGACAT	602		
DB	858	GCCCTGGTAAATGCCAGTGCAAGATGACTATACCGAGGCGCACAGCGCTCTGACAT	917		
QY	603	CGCATTTGAGAGAGGAGTCTGCAAGTGTGAAGCTCTCTGTTGAGAAATGGGGCCAATGT	662		
DB	918	CGCATTTGAGAGAGGAGTCTGCAAGTGTGAAGCTCTCTGTTGAGAAATGGGGCCAATGT	977		
QY	663	GCATGCCGGGCTGCGGCGCTTCTTCCAGAGGGCCAAAGGACTTGTCTTTATTTCCG	722		
DB	978	GCATGCCGGGCTGCGGCGCTTCTTCCAGAGGGCCAAAGGACTTGTCTTTATTTCCG	1037		
QY	723	TGAGTACCTCTCTTTTGGCGCTTGCAACAGAGTGGATGGTGAAGTACCTCT	782		
DB	1038	TGAGTACCTCTCTTTTGGCGCTTGCAACAGAGTGGATGGTGAAGTACCTCT	1097		
QY	783	GGAGAACCCACACAGCGCGGCGCTGCGAGGCACTGACTCCAGGGCCAAACAGTCCCT	842		
DB	1098	GGAGAACCCACACAGCGCGGCGCTGCGAGGCACTGACTCCAGGGCCAAACAGTCCCT	1157		
QY	843	GCATGCCCTAGTATGATCTCGGACAACTCAGCTGAGAAATTTGCACTGTGTGACAGCAT	902		
DB	1158	GCATGCCCTAGTATGATCTCGGACAACTCAGCTGAGAAATTTGCACTGTGTGACAGCAT	1217		
QY	903	GTATGATGGGCTCTCCAGTGGGGCGCGCTCTGCCCTACCGTGCAGCTTGAGGACAT	962		
DB	1218	GTATGATGGGCTCTCCAGTGGGGCGCGCTCTGCCCTACCGTGCAGCTTGAGGACAT	1277		
QY	963	CCGCAACTGCAAGGATCTCAGCTCTGAGCTGGCGCCCAAGGAGGCGCAAGATCGAGAT	1022		

DB	1278	CCGCAAACTGCAAGGATCTCACGCCCTCTGAAGCTGGCCGCCAAAGGAGGCGAAGATCGAGAT	1337		
QY	1023	TTTTCAGGACATCTCTGACGCGGAGTTTTCAGGACTGAGCCACCTTTTCCGAAAGTTCCAC	1082		
DB	1338	TTTTCAGGACATCTCTGACGCGGAGTTTTCAGGACTGAGCCACCTTTTCCGAAAGTTCCAC	1397		
QY	1083	CGAGTGGTCTATAGGCGCTGTCCGGGTGTGGTGTATGACCTGGGCTTCTGTGTGACAGCTG	1142		
DB	1398	CGAGTGGTCTATAGGCGCTGTCCGGGTGTGGTGTATGACCTGGGCTTCTGTGTGACAGCTG	1457		
QY	1143	TGAGGGAATCAGTGTCTGAGATCAATTCCTTTCAATTCGACAGAGCCGCGACGACACCG	1202		
DB	1458	TGAGGGAATCAGTGTCTGAGATCAATTCCTTTCAATTCGACAGAGCCGCGACGACACCG	1517		
QY	1203	AATGGTGTGTTTTGGAGCCCTGAAACAACTGCTGCAAGGCGAAATGGGATCTGCTCATCCC	1262		
DB	1518	AATGGTGTGTTTTGGAGCCCTGAAACAACTGCTGCAAGGCGAAATGGGATCTGCTCATCCC	1577		
QY	1263	CAAGTTCTTTCTTAAACTTCTGTGTAACTGTGATCTATCATGTTTCAATTCACCGCTGTTC	1322		
DB	1578	CAAGTTCTTTCTTAAACTTCTGTGTAACTGTGATCTATCATGTTTCAATTCACCGCTGTTC	1637		
QY	1323	CTACCATCAGCCTTACCTGAAAGAGCAGGCGCGCCCTCACCTGAAAGCGGAGGTGGAAA	1382		
DB	1638	CTACCATCAGCCTTACCTGAAAGAGCAGGCGCGCCCTCACCTGAAAGCGGAGGTGGAAA	1697		
QY	1383	CTCCATGCTGTCAGCGGCGCACATCTTATCTCTGCTAGGGGGATCTACCTCTCTGTGGG	1442		
DB	1698	CTCCATGCTGTCAGCGGCGCACATCTTATCTCTGCTAGGGGGATCTACCTCTCTGTGGG	1757		
QY	1443	CCAGCTGTGGTACTTCTGCGGCGCCACGCTGTTTCACTGTGATCTCGTTTCAATAGACGCTA	1502		
DB	1758	CCAGCTGTGGTACTTCTGCGGCGCCACGCTGTTTCACTGTGATCTCGTTTCAATAGACGCTA	1817		
QY	1503	CTTTGAAATCTCTTCTGTTCCAGGCGCTGCTCAAGTGGTGTCCAGGCTGTGTGTTT	1562		
DB	1818	CTTTGAAATCTCTTCTGTTCCAGGCGCTGCTCAAGTGGTGTCCAGGCTGTGTGTTT	1877		
QY	1563	CTTGCGCATCGAGTGTGTACCTGCGCCCTGCTGTGTGTCTGCGCTGTGGCTGGCTGAA	1622		
DB	1878	CTTGCGCATCGAGTGTGTACCTGCGCCCTGCTGTGTGTCTGCGCTGTGGCTGGCTGAA	1937		
QY	1623	CTTGCTTTACTATPACGTTGGCTTCCAGCACACAGGCACTACAGTGTCTATGATCCAGAA	1682		
DB	1938	CTTGCTTTACTATPACGTTGGCTTCCAGCACACAGGCACTACAGTGTCTATGATCCAGAA	1997		
QY	1683	GCTCATCTGCGGGAAGCTGCTGCGCTTCTTCTGATCTACTAGTCTTCTTTTGGCTT	1742		
DB	1998	GCTCATCTGCGGGAAGCTGCTGCGCTTCTTCTGATCTACTAGTCTTCTTTTGGCTT	2057		
QY	1743	CGCTGTAGCCCTGCTGAGCCTGAGCCAGGAGGCTTGGCGCGCCGAAAGCTCTTACAGGCC	1802		
DB	2058	CGCTGTAGCCCTGCTGAGCCTGAGCCAGGAGGCTTGGCGCGCCGAAAGCTCTTACAGGCC	2117		
QY	1803	CAATGGCCACAGAGTGTGAGCCCATGGAGGGAAGAGGGAACAGGGGCCAACCGGGGCCA	1862		
DB	2118	CAATGGCCACAGAGTGTGAGCCCATGGAGGGAAGAGGGAACAGGGGCCAACCGGGGCCA	2177		
QY	1863	GTACAGGGGTATCTCTGGAAGCCCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGGCGA	1922		
DB	2178	GTACAGGGGTATCTCTGGAAGCCCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGGCGA	2237		
QY	1923	GCTGGCCTTCCAGGAGCAGCTGCACTTCCGCGCATGTGTGCTGTGCTGTGCTGGGCTA	1982		
DB	2238	GCTGGCCTTCCAGGAGCAGCTGCACTTCCGCGCATGTGTGCTGTGCTGTGCTGGGCTA	2297		
QY	1983	CGTGTGCTCACCTTACCTCTGTGTCTCAATGTCTCATGTCTCATGTCTCATGTCTCATGTCT	2042		
DB	2298	CGTGTGCTCACCTTACCTCTGTGTCTCAATGTCTCATGTCTCATGTCTCATGTCTCATGTCT	2357		
QY	2043	CAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGCGAAGAGGCATCTCTGTCTCT	2102		
DB	2358	CAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGCGAAGAGGCATCTCTGTCTCT	2417		

QY	301	CCGGATCCAAACCGATTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCC	360	1381	AACTCCATGCTGCTGACGGGCCACATCCTTATCTCTGCTAGGGGGGATCTACCTCTCTCGTG	1440
DB	587	CCGGATCCAAACCGATTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCC	646	1664	AACTCCATGCTGCTGACGGGCCACATCCTTATCTCTGCTAGGGGGGATCTACCTCTCTCGTG	1723
QY	361	GAGGATCTGGCTCGGACTTCCAGAGTACCTGAGCAAGACAGCAAGTACCTCACCGGACTCG	420	1441	GGCCAGCTGTGTGTAATCTTCTGGCGGGGCCACGTTTCATCTGGATCTCTGTTCAATAGACAGC	1500
DB	647	GAGGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACAGCAAGTACCTCACCGGACTCG	706	1724	GGCCAGCTGTGTGTAATCTTCTGGCGGGGCCACGTTTCATCTGGATCTCTGTTCAATAGACAGC	1783
QY	421	GAATACACAGAGGGCTCCACAGGTAAAGCGTGCTGTGAAGGCTGTGCTGAAACCTTAAG	480	1501	TACTTTGAAATCCTCTTCTGTTCCAGGCCCTGCTCACAGTGGTGTCCAGGTGCTGTGT	1560
DB	707	GAATACACAGAGGGCTCCACAGGTAAAGCGTGCTGTGAAGGCTGTGCTGAAACCTTAAG	766	1784	TACTTTGAAATCCTCTTCTGTTCCAGGCCCTGCTCACAGTGGTGTCCAGGTGCTGTGT	1843
QY	481	GACGGAGTCAATGCCCTGCAATTCGCACTGTGCAAGCTCTGATGAAGGCTGTGCTGAAACCTTAAG	540	1561	TTCTCGGCCCATCAGAGTGTACCTGCCCTGCTGTGTCTGCGCTGTGTGCTGGGCTGGCTG	1620
DB	767	GACGGGTCATATGCCCTGCAATTCGCACTGTGCAAGCTCTGATGAAGGCTGTGCTGAAACCTTAAG	826	1844	TTCTCGGCCCATCAGAGTGTACCTGCCCTGCTGTGTCTGCGCTGTGTGCTGGGCTGGCTG	1903
QY	541	CAGCCCTGTGTAATGCCCCAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCAC	600	1621	AACTGCTTTTACTATACACGTGGCTTTCCAGACACACAGGCATCTACAGTGTCAATGATCCAG	1680
DB	827	CAGCCCTGTGTAATGCCCCAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCAC	886	1904	AACTGCTTTTACTATACACGTGGCTTTCCAGACACACAGGCATCTACAGTGTCAATGATCCAG	1963
QY	601	ATGCCATTGAGAAGAGGAGTCTGCAGTGTGAAAGCTCTCTGGTGGAGAAATGGGGCCAAT	660	1681	AAAGTCAATCCTCGGGGACCTGCTGGGCTTCTTCTGATCTTCTTAGTCTTCTTTTCGGC	1740
DB	887	ATGCCATTGAGAAGAGGAGTCTGCAGTGTGAAAGCTCTCTGGTGGAGAAATGGGGCCAAT	946	1964	AAAGTCAATCCTCGGGGACCTGCTGGGCTTCTTCTGATCTTCTTAGTCTTCTTTTCGGC	2023
QY	661	GTGCATGCCCGGGCTGCGGCCGCTTCTTCCAGAGGGCCCAAGGACTTGTCTTTTATTTTC	720	1741	TTCTCGGTAGCCCTGGTGAAGCTGTGAGCCCTGAGCCAGGAGGCTTGGGCGCCCGAAGCTCTACAGGC	1800
DB	947	GTGCATGCCCGGGCTGCGGCCGCTTCTTCCAGAGGGCCCAAGGACTTGTCTTTTATTTTC	1006	2024	TTCTCGGTAGCCCTGGTGAAGCTGTGAGCCCTGAGCCAGGAGGCTTGGGCGCCCGAAGCTCTACAGGC	2083
QY	721	GGTGAGTACCCCTCTCTTTGGCGGCTTGACCAAGCAGTGGATGTGTTAAGCTACCTC	780	1801	CCCAATGCCACAGAGTCACTGTCAGGCCCATGGAGGGAACAGAGGACAGAGGCGCAACGGGGCC	1860
DB	1007	GGTGAGTACCCCTCTCTTTGGCGGCTTGACCAAGCAGTGGATGTGTTAAGCTACCTC	1066	2084	CCCAATGCCACAGAGTCACTGTCAGGCCCATGGAGGGAACAGAGGACAGAGGCGCAACGGGGCC	2143
QY	781	CTGGAGAAACCAACACAGCCCGCAGCTTCAGGCCCACTGACTCCACAGGGCAACACAGTC	840	1861	CAGTACAGGGGTATCTCTGGAAGCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGGC	1920
DB	1067	CTGGAGAAACCAACACAGCCCGCAGCTTCAGGCCCACTGACTCCACAGGGCAACACAGTC	1126	2144	CAGTACAGGGGTATCTCTGGAAGCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGGC	2203
QY	841	CTGCATGCCCTAGTGATGATCTCGGACAACTCAGCTGAGAACATTTGACTGTGTGACGAC	900	1921	GAGCTGGCTTCCAGGAGCAGCTGCATTTCCGCGGATGCTGTGCTGTGCTGTGCTGGCC	1980
DB	1127	CTGCATGCCCTAGTGATGATCTCGGACAACTCAGCTGAGAACATTTGACTGTGTGACGAC	1186	2204	GAGCTGGCTTCCAGGAGCAGCTGCATTTCCGCGGATGCTGTGCTGTGCTGTGCTGGCC	2263
QY	901	ATGTATGATGGGCTCTCAGCTGGGGCGGCTCTGCCCTACCGTGACGCTTGGAGC	960	1981	TAGCTGCTGCTCACCTTACATCTCTGTCTCAACATGCTCATCGCCCTCATGAGCGAGACC	2040
DB	1187	ATGTATGATGGGCTCTCAGCTGGGGCGGCTCTGCCCTACCGTGACGCTTGGAGC	1246	2264	TAGCTGCTGCTCACCTTACATCTCTGTCTCAACATGCTCATCGCCCTCATGAGCGAGACC	2323
QY	961	ATCCGAACTTGACGATCTCAGCCCTCTGAAGCTGGCCCGCCAGAGGAGGCAAGATCGAG	1020	2041	GTCAAACAGTGTGCTGCTGACAGCTGGAAGCATCTGGAAGCTGCAAGAACCATCTCTGTC	2100
DB	1247	ATCCGAACTTGACGATCTCAGCCCTCTGAAGCTGGCCCGCCAGAGGAGGCAAGATCGAG	1306	2324	GTCAAACAGTGTGCTGCTGACAGCTGGAAGCATCTGGAAGCTGCAAGAACCATCTCTGTC	2383
QY	1021	ATTTTCAGGCACATCTGACGCGGAGTTTTCAGGACTGAGCCACCTTTTCCGAAAGTTTC	1080	2101	CTGGAGATGGAGAAATGGCTATTGCTGTGTCAGGAAGACAGCGGCAGGTGTGATGCTG	2160
DB	1307	ATTTTCAGGCACATCTGACGCGGAGTTTTCAGGACTGAGCCACCTTTTCCGAAAGTTTC	1366	2384	CTGGAGATGGAGAAATGGCTATTGCTGTGTCAGGAAGACAGCGGCAGGTGTGATGCTG	2443
QY	1081	ACCGAGTGTGCTATGGGCTGTCCGGTGTCTGCTGTATGACCTGGCTTCTGTGGACGC	1140	2161	ACCGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGTGCTTCAAGGTTGAGGAG	2220
DB	1367	ACCGAGTGTGCTATGGGCTGTCCGGTGTCTGCTGTATGACCTGGCTTCTGTGGACGC	1426	2444	ACCGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGTGCTTCAAGGTTGAGGAG	2503
QY	1141	TGTGAGGAGAACTCAGTGTGGAGATCATTTGCCCTTTTCAATTGCAAGAGCCCGCACACAC	1200	2221	GTGAACTGGGCTTTCATGGAGCAGACGCTGCTTACCGCTGTGTGAGGACCCGTCAGGGGCA	2280
DB	1427	TGTGAGGAGAACTCAGTGTGGAGATCATTTGCCCTTTTCAATTGCAAGAGCCCGCACACAC	1486	2504	GTGAACTGGGCTTTCATGGAGCAGACGCTGCTTACCGCTGTGTGAGGACCCGTCAGGGGCA	2563
QY	1201	CGAATGTGTGTTTGGAGCCCTGAAACAACTGCTGACGGCGAAATGGGATCTGCTCATC	1260	2281	GGTGTCCCTCGAACTCTCGAGAACCTGTCTGGCTTCCCTCCCAAGGAGGATGAGGAT	2340
DB	1487	CGAATGTGTGTTTGGAGCCCTGAAACAACTGCTGACGGCGAAATGGGATCTGCTCATC	1546	2564	GGTGTCCCTCGAACTCTCGAGAACCTGTCTGGCTTCCCTCCCAAGGAGGATGAGGAT	2623
QY	1261	CCCAAGTCTCTTAAATCTCTGTGTAAATCTGATCTACATGTTTCATCTTCAACGCTGTT	1320	2341	GGTGTCCCTCGAAGAAATATGTGCCCGTCCAGTCTCTCCAGTCCAACTGATGGCCGAGA	2400
DB	1547	CCCAAGTCTCTTAAATCTCTGTGTAAATCTGATCTACATGTTTCATCTTCAACGCTGTT	1606	2624	GGTGTCCCTCGAAGAAATATGTGTGCCCGTCCAGTCTCTCCAGTCCAACTGATGGCCGAGA	2683
QY	1321	GCCTTACCATTACCTCTGAAGAGCAGCGCCCGCTCACCTTGAAGCGGAGTTTGA	1380	2401	TGACAGCAGAGGCGCAGAGGACAGAGCAGAGGATCTTTTCCAAACCATCTGCTGGCTCTG	2460
DB	1607	GCCTTACCATTACCTCTGAAGAGCAGCGCCCGCTCACCTTGAAGCGGAGTTTGA	1663	2684	TGACAGCAGAGGCGCAGAGGACAGAGCAGAGGATCTTTTCCAAACCATCTGCTGGCTCTG	2743
				2461	GGTCCCCAGT	2469

PRIOR APPLICATION NUMBER: 60/056,636		Matches 2365; Conservative 10; Mismatches 5; Indels 70; Gaps 4;
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,874		QY 20 TGGGAGGAGACAGAGACCCTTGACATCTCCATCTGCACAGAGGTCTCTGGCTGGACCGAGC 79
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,910		Db 319 TGGGAGGAGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGGTCTCTGGCTGGACCGAGC 378
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,864		QY 80 AGCCTCTCTCTCTAGGATGACCTCACCTCCAGCTCTCCAGTCTTCCAGTCTTTCAGGTTGGAGACAT 139
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,631		Db 379 AGCCTCTCTCTCTAGGATGACCTCACCTCCAGCTCTCCAGTCTTCCAGTCTTTCAGGTTGGAGACAT 438
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,845		QY 140 TAGATGGAGGCCAAGAAGATGGCTCTGAGGCGGACAGAGGAAAGCTGGATTTTGGAGCG 199
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,892		Db 439 TAGATGGAGGCCAAGAAGATGGCTCTGAGGCGGACAGAGGAAAGCTGGATTTTGGAGCG 498
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/057,761		QY 200 GGCTGCTCCCATNGAGTCAAGTTCCAGGGGAGGACCGGAAATTCGCCCTTCAGATAA 259
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/047,595		Db 499 GGCTGCTCCCATNGAGTCAAGTTCCAGGGGAGGACCGGAAATTCGCCCTTCAGATAA 558
PRIOR FILING DATE: 1997-05-23		
PRIOR APPLICATION NUMBER: 60/047,599		QY 260 GAGTCAACCTCAACTACCGAAAGGGAACAGGTCCAGTCCAGCCGATCCAAACCCGATTTG 319
PRIOR FILING DATE: 1997-05-23		
PRIOR APPLICATION NUMBER: 60/047,588		Db 559 GAGTCAACCTCAACTACCGAAAGGGAACAGGTCCAGTCCAGCCGATCCAAACCCGATTTG 618
PRIOR FILING DATE: 1997-05-23		
PRIOR APPLICATION NUMBER: 60/047,585		QY 320 ACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCGAGGATCTGGCTGGACTTC 379
PRIOR FILING DATE: 1997-05-23		
PRIOR APPLICATION NUMBER: 60/047,586		Db 619 ACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCGAGGATCTGGCTGGACTTC 678
PRIOR FILING DATE: 1997-05-23		
PRIOR APPLICATION NUMBER: 60/047,590		QY 380 CAGAGTACTGAGCAAGACCAAGTACTCACCGACTCGGAATACACAGAGGGCTCCA 439
PRIOR FILING DATE: 1997-05-23		
PRIOR APPLICATION NUMBER: 60/047,594		Db 679 CAGAGTACTGAGCAAGACCAAGTACTCACCGACTCGGAATACACAGAGGGCTCCA 738
PRIOR FILING DATE: 1997-05-23		
PRIOR APPLICATION NUMBER: 60/047,589		QY 440 CAGGTAAGACGTGCTGATGAAGGTGTGCTCAACTTAAGGACCGAGTCAATGCTGCA 499
PRIOR FILING DATE: 1997-05-23		
PRIOR APPLICATION NUMBER: 60/047,593		Db 739 CAGGTAAGACGTGCTGATGAAGGTGTGCTCAACTTAAGGACCGAGTCAATGCTGCA 798
PRIOR FILING DATE: 1997-05-23		
PRIOR APPLICATION NUMBER: 60/047,614		QY 500 TTCTGCCACTGCTGCAGATCGACAGGGACTCTGGCAATCTCAGCCCCCTGGTAAATGCC 559
PRIOR FILING DATE: 1997-05-23		
PRIOR APPLICATION NUMBER: 60/043,578		Db 799 TTCTGCCACTGCTGCAGATCGACCGGACTCTGGCAATCTCAGCCCCCTGGTAAATGCC 858
PRIOR FILING DATE: 1997-04-11		
PRIOR APPLICATION NUMBER: 60/043,576		QY 560 AGTGACAGATGACTATTACGAGGCGCACAGCGCTCTGCACATCGCCATTGAGAAGAGA 619
PRIOR FILING DATE: 1997-04-11		
PRIOR APPLICATION NUMBER: 60/047,501		Db 859 AGTGACAGATGACTATTACGAGGCGCACAGCGCTCTGCACATCGCCATTGAGAAGAGA 918
PRIOR FILING DATE: 1997-05-23		
PRIOR APPLICATION NUMBER: 60/043,670		QY 620 GTCTGCAGTGTGAGAGTCTCTGGTGGAGAAATGGGCGCAATGTGCATGCCCGCGCTGG 679
PRIOR FILING DATE: 1997-04-11		
PRIOR APPLICATION NUMBER: 60/056,632		Db 919 GWTGCAGTGTGAGAGTCTCTGGTGGAGAAATGGGCGCAATGTGCATGCCCGGTCTGG 978
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,664		QY 680 GCGGCTTCTTCCAGAGGGGCCAAGGACCTTGCTTTTATTTTCGGTGAGCTACCCCTCTCT 739
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,876		Db 979 G-CGCTTCTTCCAGAGGGGCCAAGGACCTTGCTTTTATTTTCGGTGAGCTACCCCTCTCT 1037
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,881		QY 740 TGGCGCTTGGACCAAGCAGTGGGATGTGTAAGCTACCTCTCTGGAGAACCCACACGAGC 799
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,909		Db 1038 TGGCGCTTGGACCAAGCAGTGGGATGTGTAAGCTACCTCTCTGGAGAACCCACACGAGC 1097
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,875		QY 800 CCGCCAGCTGCAGGCGCACTGACTCCAGGGCAACACAGTCTCTGCATGCCCTAGTGATGA 859
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,862		Db 1098 CCGCCAGCTGCAGG-CAGTGACTCCAGGGCAACACAGTCTCTGCATGCCCTAGTGATGA 1156
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,887		QY 860 TCTCGGACAACTCAGCTGAGAAACATTGCACTGGTGACCAAGCATGTATGATGGGCTCTCT 919
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/056,908		Db 1157 TCTCGGACAACTCAGCTGAGAAACATTGCACTGGTGACCAAGCATGTATGATGGGCTCTCT 1216
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/048,964		QY 920 AAGCTGGGGCCCGCTCTGCCCCCTACCGTGCAGCTTGAGGACATCCGCAACCTGCAGATC 979
PRIOR FILING DATE: 1997-06-06		
PRIOR APPLICATION NUMBER: 60/057,650		Db 1217 AAGCTGGGGCCCGCTCTGCCCCCTACCGTGCAGCTTGAGGACATCCGCAACCTGCAGATC 1276
PRIOR FILING DATE: 1997-09-05		
PRIOR APPLICATION NUMBER: 60/056,884		QY 980 TCACGCCCTGTAAGCTGGCGCCCAAGGAGGCAAGATCGAGATTTTCAGGCACATCCTGC 1039
PRIOR FILING DATE: 1997-08-22		
PRIOR APPLICATION NUMBER: 60/057,669		Db 1277 TCACGCCCTGTAAGCTGGCGCCCAAGGAGGCAAGATCGAGATTTTCAGGCACATCCTGC 1336
PRIOR FILING DATE: 1997-09-05		
PRIOR APPLICATION NUMBER: 60/057,669		QY 1040 AGCGGAGTTCAGGACTGAGCCACTTTTCCCGAAAGTTCCCGAGTGTGTATGGGC 1099
PRIOR FILING DATE: 1997-09-05		
PRIOR APPLICATION NUMBER: 60/057,669		Db 1337 AGCGGAGTTCAGGACTGAGCCACTTTTCCCGAAAGTTCCCGAGTGTGTATGGGC 1396

1100 CTGTCGGGTGCTGCTGATGACCTGGCTTCTGTGACAGCTGTGAGGAGAACTCAGTGC 1159
1397 CTGTCGGGGGTGCTGCTGATGACCTGGCTTCTGTGACAGCTGTGAGGAGAACTCAGTGC 1456
1160 TGGAGATCATTTGCTTTTCATTGCAAGAGCCGACCGACACACCGAAATGGTGGTGGAGC 1219
1457 TGGAGATCATTTGCTTTTCATTGCAAGAGCCGACCGACACCGAAATGGTGGTGGAGC 1516
1220 CCTGAAACAACTGCTGACGCGAAATGGGATCTGCTCATCTCCCAAGTTCTTCTTAAACT 1279
1517 CCTGAAACAACTGCTGACGCGAAATGGGATCTGCTCATCTCCCAAGTTCTTCTTAAACT 1576
1280 TCCGTGTGATCTGATCTGATCTCATCTTTCACCGCTGTGCTTCCATCCATCAGCCTACCC 1339
1577 TCTGTGTGATCTGATCTGATCTCATCTTTCACCGCTGTGCTTCCATCCATCAGCCTACCC 1636
1340 TGAAGAAGCAGGCGCCCTTCACTGAAAGCGGAGGTTGGAACCTCCATGCTGTCACCG 1399
1637 TGAAGAAGCAGGCGCCCTTCACTGAAAGCGGAGGTTGGAACCTCCATGCTGTCACCG 1696
1400 GCCACATCTTATCTGCTAGGCGGAGTACTCTCTCTGCTGGGCGAGCTGTGATCTTCT 1459
1697 GCCACATCTTATCTGCTAGGCGGAGTACTCTCTCTGCTGGGCGAGCTGTGATCTTCT 1756
1460 GCGCGGCCACGCTTTCATCTGGATCTCGTTTCATAGACAGCTACTTTGAAATCCTCTTC 1519
1757 GCGCGGCCACGCTTTCATCTGGATCTCGTTTCATAGACAGCTACTTTGAAATCCTCTTC 1816
1520 TGTTCACAGGCGCTGCTCACAGTGTGTCCAGAGTGTGTGTTTCCTGGCCATCGAGTGT 1579
1817 TGTTCARGCCCTGCTCACAGTGTGTCCAGAGTGTGTGTTTCCTGGSCATCGAGTGT 1876
1580 ACTTGCCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1639
1877 ACTTGCCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1936
1640 GTGGCTTCACGACACAGGATCTACAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1699
1937 GTGGCTTCACGACACAGGATCTACAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1758
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1979 -----AGCCTGCTGA 1989
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1990 GCCTGAGCCAGGA-NNTTGGCGCCCCGAGTCTCTACAGGCCCAATGCCACAGAGTCAG 2048
1820 TGCAGCCATGGAGGGACAGAGGACGAGGGCAACGGGGCCAGTACAGGGGTATCTCTGG 1879
2049 TGCAGCCATGGAGGGACAGAGGACGAGGGCAACGGGGCCAGTACAGGGGTATCTCTGG 2108
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2109 AAGCCTCTTGGAGCTTCAAAATTCACCATCGGCATGGGGAGCTGGCCTTCCAGGAGC 2168
1940 AGCTGCACTTCCGGGCGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1999
2169 AGCTGCACTTCCGGGCGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2228
2000 TCCTGCTGCTCAACATGCTCATCGCCCTCATGAGGAGACCGTCAACAGTGTGCGCACTG 2059
2229 TCCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACCGTCAACAGTGTGCGCACTG 2288
2060 ACAGCTGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGCTCGAGATGGAGATGGCT 2119
2289 ACAGCTGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGCTCGAGATGGAGATGGCT 2348
2120 ATTGTGTGTGAGGAAGCAGCGGGCAGGCTGTGATGCTGTACCGTGTGGCACTAAGCCAG 2179
2349 ATTGTGTGTGAGGAAGCAGCGGGCAGGCTGTGATGCTGTACCGTGTGGCACTAAGCCAG 2408

2180 ATGGAGCCCGGATGAGCGCTGTGCTTCAAGGTGAGAGGTGAACCTGGGCTTTCATGGG 2239
2409 ATGGCAGCCCSGATGAGCGCTGTGCTTCAAGGTGAGAGGTGAACCTGGGCTTTCATGGG 2468
2240 AGCAGACGCTGCTTACGCTGTGTGAGGACCCGCTCAGGGGCGAGGTGTCCTCGAACTCTCG 2299
2469 AGCAGACGCTGCTTACGCTGTGTGAGGACCCGCTCAGGGGCGAGGTGTCCTCGAACTCTCG 2528
2300 AGAACCTCTCTCTGGCTTCCCTCCCAAGGAGGATGAGGATGGTGTCTCTGAGGAAAACT 2359
2529 AGAACCTCTCTCTGGCTTCCCTCCCAAGGAGGATGAGGATGGTGTCTCTGAGGAAAACT 2588
2360 ATGTGCCCCCTCAGCTCTCCAGTCCAACTGATGGCCCCAGATGACAGAGGAGCCAGAGG 2419
2589 ATGTGCCCCCTCAGCTCTCCAGTCCAACTGATGGCCCCAGATGACAGAGGAGCCAGAGG 2648
2420 ACNAGCAGAGGATCTTTCCAAACCACATCTGCTGGCTCTGGGGTCCCACT 2469
2649 ACAGAGCAGAGGATCTTTCCAAACCACATCTGCTGGCTCTGGGGTCCCACT 2698

RESULT 13
US-10-164-861-191
; Sequence 191, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 191
; LENGTH: 2779
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (318)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2003)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2004)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-164-861-191

Query Match 91.5%; Score 2259.2; DB 17; Length 2779;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 2365; Conservative 10; Mismatches 5; Indels 70; Gaps 4;
QY 20 TGGGAGGAAGACAGGACCCCTTGACATCTCCATCTGCAACAGAGTCTCTGGTGGACCGAGC 79
Db 319 TGGGAGGAAGACAGGACCCCTTGACATCTCCATCTGCAACAGAGTCTCTGGTGGACCGAGC 378
QY 80 AGCCTCTCTCTCTAGATGACCTCACCTCCAGCTCTCCAGTTTTCAGGTTGGAGACAT 139
Db 379 AGCCTCTCTCTCTAGATGACCTCACCTCCAGCTCTCCAGTTTTCAGGTTGGAGACAT 438
QY 140 TAGATGAGGCCAAGAGATGGCTCTCAGGCGGACAGAGAAAGCTGGATTTTGGGAGCG 199
Db 439 TAGATGAGGCCAAGAGATGGCTCTCAGGCGGACAGAGAAAGCTGGATTTTGGGAGCG 498
QY 200 GGCTGCTCTCCATGGAGTCAAGTTTCAGGGGCGAGGACCGGAAATTCGCCCTCAGATAA 259

QY 2420 ACAGAGCAGGAGTCTTCCAAACACATCTGCTGGCTCTGGGTCCAGT 2469
Db |||||||
2649 ACAGAGCAGGAGTCTTCCAAACACATCTGCTGGCTCTGGGTCCAGT 2698
Db |||||||
RESULT 14
US-09-809-391-314
; Sequence 314, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002p2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 314
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-314
Query Match 83.5%; Score 2061.8; DB 10; Length 2860;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 2364; Conservative 4; Mismatches 31; Indels 86; Gaps 20;
QY 3 CGAGGCGCAGCGCAGCTGGGAGGAGACAGCAGGACCTTTGACATCTCCATCTGCACAGG 62
Db 325 CAACACCGACCGCAGCTCTGCGGAGGAGACAGGACCTTGACATCTCCATCTGCACAGG 384
QY 63 TCCTGGCTGG-ACCGAGCAGCTCTCTCTCTAGGATGACCTACCTCCAGCTCTCCAG 121
Db 385 TCCTGGCTGGAAACCGAGCAGCTCTCTCTCTAGGATGACCTACCTCCAGCTCTCCAG 444
QY 122 TTTTCAGTTGGAGACATAGATCGAGGCCAAGAGATGCTCTGAGCGGACAGAGAA 181
Db 445 TTTTCAGTTGGAGACATAGATCGAGGCCAAGAGATGCTCTGAGCGGACAGAGAA 504
QY 182 AGCTGGATTTTGGAGCGGCTGCTCCATGGAGTCAAGTTCAGGCGGAGGACCGGA 241
Db 505 AGCTGGATTTTGGAGCGGCTGCTCCATGGAGTCAAGTTCAGGCGGAGGACCGGA 564
QY 242 AATTGCGCCC-TCAGATAAGAGTCAACCT-CAACTACCGAAAGGAAACAGGTGCGAGTCA 299
Db 565 AATTGCGCCCTTCAGATAAGAGTCAACCTCAACTACCGAAAGGAAACAGGTGCGAGTCA 624
QY 300 GCCGATCCAAACCGATTGACCGAGATCGGCTCTTCAATCGGCTCTCCCGGGGTGCC 359
Db 625 GCCGATCCAAACCGATTGACCGAGATCGGCTCTTCAATCGGCTCTCCCGGGGTGCC 684
QY 360 CGAGGATCTGGCTGACCTTCAGAGTACCTCAGCAAGACAGCAAGTACCTCACCGACT- 418
Db 685 CGAGGATCTGGCTGACCTTCAGAGTACCTCAGCAAGACAGCAAGTACCTCACCGACTT 744
QY 419 -CGGAATACACAGAGGCTCCACAGGTAAAGCTGCTGTAGTGAAGGCTGTGCTG-AACT 476
Db 745 CGGAATACACAGAGGCTCCACAGGTAAAGCTGCTGTAGTGAAGGCTGTGCTGAAACCT 803
QY 477 TAAGAACGAGGTCAATGCTGTGATTCGTCAGATCGACAGGATCTGCGAA 536
Db 804 TAAGAACGAGGTCAATGCTGTGATTCGTCAGATCGACAGGATCTGCGAA 863
QY 537 TCCTCAGCCCTGGTAAATGCCAGTGCACAGATGACTATTACCGAGGCCACAGGCTCT 596
Db |||||||

Db 864 TCCTCAGCCCTCGTAAATGCCAGTGCGACAGATGACTATTACCGAGGCCACAGCGCTCT 923
QY 597 GCACATCGCATTTGAG-AAGAGGAGTCTGACGTGTGTGAAGCTCTCTGGTGGAGAAATGGG 655
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924 GCACATCGCCATTTGAGAAAGAGAGTCTGACGTGTGTGAAGCTCTCTGGTGGAGAAATGGG 983
QY 656 CCAATGTGCATCCCGGGCTCGGGCGCTTTCTTCAGAAAGGGCCAAAGGGAATTGCTTTT 715
Db 984 CCAATGTGCATCCCGGGCTCGGGCGACTTCTTCAGAAAGGGCCAAAGGGAATTGCTTTT 1043
QY 716 ATTTGGGTGAGTACCCCTCTTTTGGCGCTTGGACCAAGCAGTGGGATGTGTAAGCT 775
Db 1044 ATTTGGGTGAGTACCCCTCTTTTGGCGCTTGGACCAAGCAGTGGGATGTGTAAGCT 1103
QY 776 ACCTCTCGAGAAACCCACACAGCCGCGCAGCTGCGAGGCCACTGACTCCAGGGCAACA 835
Db 1104 ACCTCTCGAGAAACCCACACAGCCGCGCAGCTGCGAGGCCACTGACTCCAGGGCAACA 1163
QY 836 CAGTCTCTGCATGCCCTAGT-GATGATCTCGGACAACTCAGCTGAGAACATTTGCACTGGTG 894
Db 1164 CAGTCTCTGCATGCCCTAGTGGATGATCTCGGACAACTCAGCTGAGAACATTTGCACTGGTG 1223
QY 895 ACCAGCATGTATGATGGGCTCTTCCAAAGCTGGGGCCGCGC-TCCTGCCCTACCTGCAAGCT 953
Db 1224 ACCAGCATGTATGATGGGCTCTTCCAAAGCTGGGGCCGCGCCTCTGCCCCTACCCTGCAAGCT 1283
QY 954 TGAGGACATCCGCAACCTGCAAGGATCTCAGCGCTCTGAAGCTGGCGCCCAAGGAGGCA 1013
Db 1284 TGAGGACATCCGCAACCTGCAAGGATCTCAGCGCTCTGAAGCTGGCGCCCAAGGAGGCA 1343
QY 1014 GATCGAGATTTTCAGGCACATCTCGAGGGGAGTTTTCAGACTGAGCCACCTTTCCCG 1073
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QY 1074 AAGATTACCGAGTGTGATGGGCTCTGCGGGTGTGCTGTATGACCTGCTGCTCT 1133
Db 1404 AAGATTACCGAGTGTGATGGGCTCTGCGGGTGTGCTGTATGACCTGCTGCTCT 1463
QY 1134 GGCAGCTGTGAGGAGAACTCAGTGTGGAGATCATTTGCCCTTTCATTGCAAGAGCCGCA 1193
Db 1464 GGCAGCTGTGAGGAGAACTCAGTGTGGAGATCATTTGCCCTTTCATTGCAAGAGCCGCA 1523
QY 1194 CCGACACCGAATGGTGGTGGAGCCCTGAAACAACTGCTGAGCGGAAATGGGATCT 1253
Db 1524 CCGACACCGAATGGTGGTGGAGCCCTGAAACAACTGCTGAGCGGAAATGGGATCT 1583
QY 1254 GCTCATCCCAAGTTCTTTAACTTCTTAACTTCTTAACTTCTTAACTTCTTAACTTCT 1313
Db 1584 GCTCATCCCAAGTTCTTTAACTTCTTAACTTCTTAACTTCTTAACTTCTTAACTTCT 1643
QY 1314 CGCTGTGCTTACCATCGAGCTACCTGAAAGAGCAGCGCCCTCACCTGAAAGCGGA 1373
Db 1644 CGCTGTGCTTACCATCGAGCTACCTGAAAGAGCAGCGCCCTCACCTGAAAGCGGA 1703
QY 1374 GGTGGAAACTCCATGCTGCTGAGCGGCCACATCTTTATCTGCTAGGGGGAATCTACCT 1433
Db 1704 GGTGGAAACTCCATGCTGCTGAGCGGCCACATCTTTATCTGCTAGGGGGAATCTACCT 1763
QY 1434 CTTGCT-GGGCAGCTGTGTTACTTCTGCGGGCCACAGTGTTCATCTGGATCTCGTTCA 1492
Db 1764 CTTGCTGGGGCCAGCTGTGTTACTTCTGCGGGCCACAGTGTTCATCTGGATCTCGTTCA 1823
QY 1493 TAGACAGTACTTTT-GAAATCTCTTCTGTTTCCAGGCCCTGCG-TCACAGTGGTGTCCCA 1550
Db 1824 TAGACAGTACTTTTGGAAATCTCTTCTGTTTCCAGGCCCTGCTTTCACAGTGGTGTCCCA 1883
QY 1551 GGTGCTGTGTTTCTT-GGCCATCGAGTGGTACTCTGCCCTGCTGTTGTGTGCGGTGGT-G 1608
Db 1884 GGTGCTGTGTTTCTTGGGCCATCGAGTGGTACTCTGCCCTGCTGTTGTGTGCGGTGGT 1943
QY 1609 CTGGGCTGGGTGAACCTGCTTTACT-ATACAGTGGG-TTCCAGCACACAGGCATCTACA 1666
Db 1944 CTGGGCTGGGTGAACCTGCTTTACTAATACAGTGGGTTTCCAGCACACAGGC----- 1996

QY 1667 GTGTCAATCCAGAAAGTCACTCCGCGGACCTGCTGGCTTCCCTTCTGATCTACTTAG 1726
Db 1997 -----AG 1998
QY 1727 TCTTCTCTTTTCGGCTTCGTGTAGCCCTGTGAGCCTGAGCCAGGAGGCTTGGCGCCCG 1786
Db 1999 TCTACAGTTTCATGWTCCCTGAAGCCCTGTGAGCCTGAGCCAGGAGGCTTGGCGCCCG 2058
QY 1787 AAGCTCTTACAGCCCTCATGCCACAGAGTCACTGAGCCCATGGAGGGACAGGAGAGC 1846
Db 2059 AAGCTCTTACAGCCCTCATGCCACAGAGTCACTGAGCCCATGGAGGGACAGGAGAGC 2118
QY 1847 AGGGCAACGGGCCCCAGTACAGGGGTATCTGGAAGCTCTTGGAGCTTCCAAATTTCA 1906
Db 2119 AGGGCAACGGGCCCCAGTACAGGGGTATCTGGAAGCTCTTGGAGCTTCCAAATTTCA 2178
QY 1907 CCATCGCATGGCGAGCTGGCTTCCAGGAGCAGCTGCATTTCCGCGGCATGGTCTGC 1966
Db 2179 CCATCGCATGGCGAGCTGGCTTCCAGGAGCAGCTGCATTTCCGCGGCATGGTCTGC 2238
QY 1967 TGTGTCTGTGGCTACGTCTGCTCACTACATCTCTGTGCTCAACATGCTCATCGCCC 2026
Db 2239 TGTGTCTGTGGCTACGTCTGCTCACTACATCTCTGTGCTCAACATGCTCATCGCCC 2298
QY 2027 TCATGAGCAGAGCCGTCAACAGTGTGCCACTGCACAGCTGGAGCATCTGGAAGCTCAGA 2086
Db 2299 TCATGAAGCGAAC - GTACAGTGTGCCACTGCACAGCTGGAGCATCTGGAAGCTCAGA 2356
QY 2087 AAGCCATCTCTGTCTGGAGATGGAAATGGCTATTGGTGTGTCAGGAAGAACGAGCGGG 2146
Db 2357 AAGCCATCTCTGTCTGGAGATGGAAATGGCTATTGGTGTGTCAGGAAGAACGAGCGGG 2416
QY 2147 CAGGTGTGATGTGACCGTTTGGCACTAAG - CCAGATGGCAGCCCGGATGAGCGCTGGTGC 2205
Db 2417 CAGGTGTGATGTGACCGTTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGGTGC 2476
QY 2206 TTCAAGGTGAGAGAGTGAATGGCTTCAT - GGHAGCAGACGCTGCTACGCTGTGTGA 2264
Db 2477 TTCAAGGTGAGAGAGTGAATGGCTTCATGAGGAGCAGACGCTGCTACGCTGTGTGA 2536
QY 2265 GGACCCGTACAGGCGAGTGTCTCCTCGAACTCTCGAAACCTGTCTGGCTTCCCTCC 2324
Db 2537 GGACCCGTACAGGCGAGTGTCTCCTCGAACTCTCGAAACCTGTCTGGCTTCCCTCC 2596
QY 2325 CAAGGAGATGAGGATGGTCCCTCTGAGGAAAATATGTGCCGTCCAGCTCTCCAGTC 2384
Db 2597 CAAGGAGATGAGGATGGTCCCTCTGAGGAAAATATGTGCCGTCCAGCTCTCCAGTC 2656
QY 2385 CAACCTGATGCCCATGATGACGAGGAGGCGCAGAGGACAGGACAGGATCTTTCCAAACCA 2444
Db 2657 CAACCTGATGCCCATGATGACGAGGAGGCGCAGAGGACAGGACAGGATCTTTCCAAACCA 2716
QY 2445 CATCTGCTGCTCTGGGGTCCCACT 2469
Db 2717 CATCTGCTGCTCTGGGGTCCCACT 2741

RESULT 15
US-09-882-171-314
; Sequence 314, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493

; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
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; PRIOR APPLICATION NUMBER: 60/047,502
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; PRIOR APPLICATION NUMBER: 60/047,617
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; PRIOR APPLICATION NUMBER: 60/047,618
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; PRIOR APPLICATION NUMBER: 60/047,503
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; PRIOR APPLICATION NUMBER: 60/047,581
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; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,613
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; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,674
; PRIOR FILING DATE: 1997-04-11

Qy	419	-CGAATACACAGAGGGCTCCACAGGTAAGACGTGCCTGTGATGAAGGCTGTGCTG- AACCT	476
Db	745	CGGAAATACACAGAGGGCTCCACAGGTAAGACG- GCCTGATGAAGGCTGTGCTGAAACCT	803
Qy	477	TAAGGACGGAGTCAATGCTGCAATCTGCGCACTGCTGCAGATCGACAGGGAATCTGCGAA	536
Db	804	TAAGGACGGGGTCAATGCTGCAATCTGCGCACTGCTGCAGATCGACCGGGAATCTGCGAA	863
Qy	537	TCCTCAGCCCTCGTAAATGCCAGTCACAGATGACTATTACCGAGGGCCACAGCGCTCT	596
Db	864	TCCTCAGCCCTCGTAAATGCCAGTCGACAGATGACTATTACCGAGGGCCACAGCGCTCT	923
Qy	597	GCACATCGCCCATTCAG- AAGAGGAGTCTGCAGTGTGTGAAGCTCTCTGTTGGAGAAATCGGG	655
Db	924	GCACATCGCCATTGAGAAAGAGGAGTCTGCAGTGTGTGAAGCTCTCTGTTGGAGAAATCGGG	983
Qy	656	CCAATGTGCATCCCGGGCTGCGGGCCGCTTCTTCAGAGGGGCCAAGGGAATTCGCTTTT	715
Db	984	CCAATGTGCATCCCGGGTCTGCGGGCACTTTCTTCAGAGGGGCCAAGGGAATTCGCTTTT	1043
Qy	716	ATTTTCGGTGAAGTACCCCTCTCTTTTGGCCGCTTGACACAAAGCAGTGGGATGTGGTAAAGCT	775
Db	1044	ATTTTCGGTGAAGTACCCCTCTCTTTTGGCCGCTTGACACAAAGCAGTGGGATGTGGTAAAGCT	1103
Qy	776	ACCTCTCTGGAGAACCCACACACAGCCCGCAGCCTTCGAGGGCCACTGACTCCGAGGGCAACA	835
Db	1104	ACCTCTCTGGAGAACCCACACACAGCCCGCAGCCTTCGAGGGCCACTGACTCCGAGGGCAACA	1163
Qy	836	CAGTCTCTGCATGCCCTAGT- GATGATCTCGGACAACTCAGCTGAGACATTTGCACTCGGTG	894
Db	1164	CAGTCTCTGCATGCCCTAGTGGATGATCTCGGACAACTCAGCTGAGACATTTGCACTCGGTG	1223
Qy	895	ACCAGCATGTATGATGGGCTCTCCAAAGCTGGGGCCGCC- TCTGCCCCTACCGTGCAGCT	953
Db	1224	ACCAGCATGTATGATGGGCTCTCCAAAGCTGGGGCCGCC- TCTGCCCCTACCGTGCAGCT	1283
Qy	954	TGAGGACATCCGCAACCTGCAGGATCTCACGCCCTCTGAAGCTGGCCGCCAAGGAGGGCAA	1013
Db	1284	TGAGGACATCCGCAACCTGCAGGATCTCACGCCCTCTGAAGCTGGCCGCCAAGGAGGGCAA	1343
Qy	1014	GATCGAGATTTTCAGGCACATCTTCGACGGGAGTTTTCAGGACTGAGCCACCTTTCCCG	1073
Db	1344	GATCGAGATTTTCAGGCACATCTTCGACGGGAGTTTTCAGGACTGAGCCACCTTTCCCG	1403
Qy	1074	AAAGTTTCAACCGAGTGTGCTATGGGCCCTGTCCGGGTGTGCTGTATGACCTGGCTTCTGT	1133
Db	1404	AAAGTTTCAACCGAGTGTGCTATGGGCCCTGTCCGGGTGTGCTGTATGACCTGGCTTCTGT	1463
Qy	1134	GGACAGCTGTGAGAGAACTCAGTGTCTGAGATCATTTGCCCTTTTCATTTCGCAAGAGCCGCA	1193
Db	1464	GGACAGCTGTGAGAGAACTCAGTGTCTGAGATCATTTGCCCTTTTCATTTCGCAAGAGCCGCA	1523
Qy	1194	CCGACACCGAATGTGTGTTTTGGAGCCCTCGAAACAACTGCTGCAGCGCAAAATGGGATCT	1253
Db	1524	CCGACACCGAATGTGTGTTTTGGAGCCCTCGAAACAACTGCTGCAGCGCAAAATGGGATCT	1583
Qy	1254	GCTCATCCCCAAGTTCTTTCTAAACTTCTGTGTAATCTGATCTACATGTTTCATCTTTCAC	1313
Db	1584	GCTCATCCCCAAGTTCTTTCTAAACTTCTGTGTAATCTGATCTACATGTTTCATCTTTCAC	1643
Qy	1314	CGCTGTTGCCCTTACCATCAGCCCTACCTGAGAGAGCAGGCCGCCCTCACCCTGAAAGCGGA	1373
Db	1644	CGCTGTTGCCCTTACCATCAGCCCTACCTGAGAGAGCAGGCCGCCCTCACCCTGAAAGCGGA	1703
Qy	1374	GTTTGGAAAATCTCCATGCTGTGACGGGCCACATCTTATCTGCTAGGGGGGATCTACCT	1433
Db	1704	GTTTGGAAAATCTCCATGCTGTGACGGGCCACATCTTATCTGCTAGGGGGGATCTACCT	1763
Qy	1434	CCTCGT- GGGCCAGCTGTGTGTTACTTCTGGGGGCCACAGTGTTCATCTGGAATCTCTGTTC	1492
Db	1764	CCTCGTGGGGCCAGCTGTGTGTTACTTCTGGGGGCCACAGTGTTCATCTGGAATCTCTGTTC	1823

QY	1493	TAGACAGCTACTTT- GAAATCTCTTCTCTCTGTTTCAGGSCCCTGC- TCACTGTGTGTCCCA	1555
DB	1824	TAGACAGCTACTTTTGGAAATCTCTCTCTCTTCCAGGSCCCTGCTTCACTGTGTGTCCCA	1883
QY	1551	GGTCTCTGTGTTTCT- GGCCATCGAGTGTGTACCTTGCCCTGCTTGTCTGTGCGTGTGT- G	1608
DB	1884	GGTCTCTGTGTTTCTGTGGCCATCGAGTGTGTACCTTGCCCTGCTTGTGTCTGTGCGTGTGTG	1943
QY	1609	CTGGGCTGGCTGAACCTGCTTTACT- ATACACGTGGC- TTCCAGCACACAGGCGATCTTACA	1666
DB	1944	CTGGGCTGGCTGAACCTGCTTTTACTAATAACAGTGGCGTTCCAGCACACAGGC-----	1996
QY	1667	GTGTCTGATCCAGAAAGTCTATCTGCGGGACCTGTGCGCTTCTTCTGATCTACTTAG	1726
DB	1997	-----AG	1998
QY	1727	TCTTCTTTTTCGGCTTCGCTGTAGCCCTGTGTAGCCCTGAGCCACAGGAGGCTTGGCGCCCG	1786
DB	1999	TCTACAGTTTCATGTTCCCTGAAGCCCTGTGTAGCCCTGAGCCAGAGGCTTGGCGCCCG	2058
QY	1787	AAGCTCTTACAGGCCCAATGCCACAGAGTCAGTGCAGCCCATGTGAGGGGACAGAGGACG	1846
DB	2059	AAGCTCTTACAGGCCCAATGCCACAGAGTCAGTGCAGCCCATGTGAGGGGACAGAGGACG	2118
QY	1847	AGGCAACGGGGCCACGTAAGGGGTATCTCTGGAAGCCTCTCTTGGAGCTCTTCAAATTTCA	1906
DB	2119	AGGCAACAGGGGCCACGTAAGGGGTATCTCTGGAAGCCTCTCTTGGAGCTCTTCAAATTTCA	2178
QY	1907	CCATCGGCATGGGCGAGCTGGCCTTCCAGGAGAGCTGCATCTCCGCGGCATGCTGCTGC	1966
DB	2179	CCATCGGCATGGGCGAGCTGGCCTTCCAGGAGAGCTGCATCTCCGCGGCATGCTGCTGC	2238
QY	1967	TGCTGTCTGTGGCCCTACGTGTGCTACCTTACATCTCTGTCTGTCTCAACATGCTCATTCGCC	2026
DB	2239	TGCTGTCTGTGGCCCTACGTGTGCTACCTTACATCTCTGTCTGTCTCAACATGCTCATTCGCC	2298
QY	2027	TCAATGAGGAGACCGTCAAACAGTGTGCCACTGCACGCTGAGCATCTGGAAGCTGCAGA	2086
DB	2299	TCAATGAGGAGAC- GTCAACAGTGTGCCACTGCACGCTGAGCATCTGGAAGCTGCAGA	2356
QY	2087	AAGCCATCTCTGTCTGTGGAGATGGCTATTGGTGGTGCAGGAAGACGACGCGG	2146
DB	2357	AAGCCATCTCTGTCTGTGGAGATGGCTATTGGTGGTGCAGGAAGACGACGCGG	2416
QY	2147	CAGTGTGTATGCTGACCGTTTGGCACTAAG- CCAGATGGCAGCCCGGATGAGCGCTGTGTC	2205
DB	2417	CAGTGTGTATGCTGACCGTTTGGCACTAAGCCCAAGTGGCAGCCCGGATGAGCGCTGTGTC	2476
QY	2206	TTCAAGGTGAGGAGGTGAACCTGGGCTTCAT- GGGAGCAGACGCTGCTACGCTGTGTGA	2264
DB	2477	TTCAAGGTGAGGAGGTGAACCTGGGCTTCATGGGAGCAGACGCTGCTACGCTGTGTGA	2536
QY	2265	GGAACCGTCAAGGGCAGGTGTCCCTGAACTCTGAGAAACCTGTCTGTGGCTTCCCTCC	2324
DB	2537	GGAACCGTCAAGGGCAGGTGTCCCTGAACTCTGAGAAACCTGTCTGTGGCTTCCCTCC	2596
QY	2325	CAAGGAGATCAGGATGGTGGCTCTGAGGAACATATGTCGCCGTCCAGCTCTTCCAGTC	2384
DB	2597	CAAGGAGATCAGGATGGTGGCTCTGAGGAACATATGTCGCCGTCCAGCTCTTCCAGTC	2656
QY	2385	CAAATGATGGCCCAAGATGCACAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCAAACA	2444
DB	2657	CAAATGATGGCCCAAGATGCACAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCAAACA	2716
QY	2445	CATCTGTGGCTCTGGGGTCCAGT	2469
DB	2717	CATCTGTGGCTCTGGGGTCCAGT	2741

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OM protein - protein search, using sw model

Run on: October 5, 2005, 11:07:29 ; Search time 82 seconds
(without alignments)

4771.079 Million cell updates/sec

Title: US-09-445-614B-2

Perfect score: 4004

Sequence: 1 MTSPPSSPPVRLTLGGQE.....EBEDGASENYPVQLQSN 764

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4004	100.0	764	2 Q9Y5S1	Q9Y5S1 homo sapien
2	3945	98.5	764	2 Q9Y670	Q9Y670 homo sapien
3	3159	78.9	756	2 Q9WTR1	Q9WTR1 mus musculus
4	3158	78.9	756	2 Q6JGX2	Q6JGX2 F-11 rat/mo
5	3158	78.9	756	2 Q99K71	Q99K71 mus musculus
6	3051.5	76.2	761	2 Q9WUD2	Q9WUD2 rattus norv
7	3041.5	76.0	761	2 Q9QVH8	Q9QVH8 rattus norv
8	3028.5	75.6	762	2 Q9JML8	Q9JML8 rattus norv
9	1694	42.3	843	2 Q8QFN9	Q8QFN9 gallus gall
10	1652	41.3	838	2 Q35433	Q35433 rattus norv
11	1652	41.3	838	2 Q9JMS7	Q9JMS7 rattus norv
12	1651.5	41.2	839	2 Q9H304	Q9H304 homo sapien
13	1649	41.2	839	2 Q8K1W1	Q8K1W1 cavia porce
14	1649	41.2	840	2 Q89711	Q89711 canis famil
15	1648.5	41.2	839	2 Q9H0G9	Q9H0G9 homo sapien
16	1646	41.1	839	2 Q8R5A3	Q8R5A3 cavia porce
17	1645.5	41.1	839	2 Q8NER1	Q8NER1 homo sapien
18	1644.5	41.0	839	2 Q9NQ74	Q9NQ74 homo sapien
19	1642.5	41.0	839	2 Q704V3	Q704V3 mus musculus
20	1639.5	40.9	839	2 Q9NY22	Q9NY22 homo sapien
21	1638.5	40.9	842	2 Q8RX08	Q8RX08 oryctolagus
22	1617.5	40.4	829	2 Q68SW0	Q68SW0 mus musculus
23	1467	36.6	852	2 Q9DF83	Q9DF83 gallus gall
24	1467	36.6	853	2 Q86YZ6	Q86YZ6 homo sapien
25	1467	36.6	871	2 Q8NDV7	Q8NDV7 homo sapien
26	1467	36.6	871	2 Q86Q92	Q86Q92 homo sapien
27	1467	36.6	871	2 Q9HBC0	Q9HBC0 homo sapien
28	1465.5	36.6	871	2 Q9ER28	Q9ER28 rattus norv
29	1464	36.6	871	2 Q9HBA0	Q9HBA0 homo sapien
30	1458.5	36.4	871	2 Q9ES76	Q9ES76 mus musculus
31	1457.5	36.4	803	2 Q96RS7	Q96RS7 homo sapien

32	1457.5	36.4	871	2 Q9EPK8	Q9EPK8 mus musculus
33	1452.5	36.3	871	2 Q9BQZ4	Q9BQZ4 mus musculus
34	1447	36.1	803	2 Q91XR5	Q91XR5 mus musculus
35	1446.5	36.1	873	2 Q9ERZ7	Q9ERZ7 mus musculus
36	1442.5	36.0	778	2 Q9JM56	Q9JM56 rattus norv
37	1261	31.5	811	2 Q8NG64	Q8NG64 homo sapien
38	1153	28.8	790	2 Q8NDW7	Q8NDW7 homo sapien
39	1153	28.8	790	2 Q8NFH2	Q8NFH2 homo sapien
40	1146	28.6	791	2 Q8NET8	Q8NET8 homo sapien
41	1143	28.5	765	2 Q8NET9	Q8NET9 homo sapien
42	1139	28.4	791	2 Q8K424	Q8K424 mus musculus
43	1112.5	27.8	528	2 Q9Z182	Q9Z182 rattus norv
44	969	24.2	511	2 Q9H303	Q9H303 homo sapien
45	933	23.3	471	2 Q9JLM0	Q9JLM0 rattus norv

ALIGNMENTS

RESULT 1				
ID	Q9Y5S1	PRELIMINARY;	PRT;	764 AA.
AC	Q9Y5S1;			
DT	01-NOV-1999 (Tremblrel. 12, Created)			
DT	01-NOV-1999 (Tremblrel. 12, Last sequence update)			
DT	25-OCT-2004 (Tremblrel. 28, Last annotation update)			
DE	Vanilloid receptor-like protein 1 (Transient receptor potential cation channel, subfamily V, member 2).			
DE	channel, subfamily V, member 2).			
GN	Names=VRL-1; Synonyms=TRPV2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=99215558; PubMed=10201375; DOI=10.1038/18906;			
RX	Caterina M.J., Rosen T.A., Tominaga M., Brake A.J., Julius D.;			
RT	"A capsaicin-receptor homologue with a high threshold for noxious heat."			
RL	Nature 398:436-441(1999).			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=22107054; PubMed=12077606; DOI=10.1038/nature00894;			
RX	Smith G.D., Gunthorpe M.J., Kelsell R.E., Hayes P.D., Reilly P.,			
RA	Racer P., Wright J.E., Jerman J.C., Walhin J.P., Ooi L., Egerton J.,			
RA	Charles K.J., Smart D., Randall A.D., Anand P., Davis J.B.;			
RT	"TRPV3 is a temperature-sensitive vanilloid receptor-like protein."			
RL	Nature 418:186-190(2002).			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Skin;			
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[4]			

Db 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAQCTDDYIRGHSALHIAIEKRSLSQCVK 180
 Qy 181 LLVENGANVHARACGRFFQKQGTCTFYFGEPLPLSLAACTKQWDVSYLLENPHOPASLOA 240
 Db 181 LLVENGANVHARACGRFFQKQGTCTFYFGEPLPLSLAACTKQWDVSYLLENPHOPASLOA 240
 Qy 241 TDSQGNVTVLHALVMI SDNSAENALTVMYDGLLOAGARLCPTVQLEDIRNLDLTPLKL 300
 Db 241 TDSQGNVTVLHALVMI SDNSAENALTVMYDGLLOAGARLCPTVQLEDIRNLDLTPLKL 300
 Qy 301 AAKEGKIEIFRHILOREFSGLSLRSKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
 Db 301 AAKEGKIEIFRHILOREFSGLSLRSKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
 Qy 361 HCKSPHRHVMVLEPLNKLLOAKWDLILPKFFLNFLCNLIYMFIFTAVAYHQTLLKQAA 420
 Db 361 HCKSPHRHVMVLEPLNKLLOAKWDLILPKFFLNFLCNLIYMFIFTAVAYHQTLLKQAA 420
 Qy 421 PHLKAEGVNSMLTGHILILGGLIYLLVGLQWYFWRHVFIIWISFIDSYFEILFLFOALL 480
 Db 421 PHLKAEGVNSMLTGHILILGGLIYLLVGLQWYFWRHVFIIWISFIDSYFEILFLFOALL 480
 Qy 481 TVVSVQLCFIAIEWILPLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRDLRLFL 540
 Db 481 TVVSVQLCFIAIEWILPLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRDMVRLV 540
 Qy 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEGDEGNGAQYRGILEASLEL 600
 Db 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEGDEGNGAQYRGILEASLEL 600
 Qy 601 FKFTIGMELAFQELHFRGMVLLLLAYVLLTYLILNMLIALMSETVNSVATDSWSIW 660
 Db 601 FKFTIGMELAFQELHFRGMVLLLLAYVLLTYLILNMLIALMSETVNSVATDSWSIW 660
 Qy 661 KLOKAI SVLEMENGYWCRKKQKQAGVMLTVGTGPDGSDPDRWCFRVEEVNWSAEQTLPT 720
 Db 661 KLOKAI SVLEMENGYWCRKKQKQAGVMLTVGTGPDGSDPDRWCFRVEEVNWSAEQTLPT 720
 Qy 721 LCBDPSGAGVPTLENVPLASPKEDBDGASEENYVPVQLQSN 764
 Db 721 LCBDPSGAGVPTLENVPLASPKEDBDGASEENYVPVQLQSN 764

RESULT 3

Q9WTR1 PRELIMINARY; PRT; 756 AA.
 AC Q9WTR1
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Growth factor regulated calcium channel.
 GN Name=Trpv2; Synonyms=GRC;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57 Black-6; TISSUE=Spleen;
 RX MEDLINE=20032759; PubMed=10559903; DOI=10.1038/11086;
 RA Kanzaki M., Zhang Y.-Q., Mashima H., Li L., Shibata H., Kojima I.;
 RT "Translocation of a calcium-permeable cation channel induced by
 RL insulin-like growth factor-I";
 RL Nat. Cell Biol. 1:165-170(1999).
 DR EMBL; AB021665; BAA78478.1; --
 DR MGD; MGI:1341836; Trpv2.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR GO; GO:0005261; F:cation channel activity; IDA.
 DR GO; GO:0009266; P:response to temperature; IDA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.

DR InterPro; IPR004729; TRPChannel.
 DR InterPro; IPR008347; Vanil_receptor.
 DR Pfam; PF00023; Ank; 4.
 DR Pfam; PF00520; Ion_trans; 1.
 DR PRINTS; PRO1415; ANKTRIN.
 DR PRINTS; PRO1768; TRPVECEPTOR.
 DR SMART; SM00248; ANK; 4.
 DR TIGRFAMs; TIGR00870; tip; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REPEAT; 1.
 DR ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 756 AA; 85964 MW; 4C037D0F6066E4C CRC64;

Query Match 78.9%; Score 3159; DB 2; Length 756;

Best Local Similarity 80.3%; Pred. No. 2.4e-215;

Matches 615; Conservative 55; Mismatches 84; Indels 12; Gaps 5;

Qy 1 MTSPTSSPVRLTETDGGQDGEADRGKLDPGSLPPMESQFQGEDRFQAFQIRVNLNY 60

Db 1 MTSASNPPAFRLTETSDGDEGSAEVNKGK----NEPPPMESPFGCEDRNFSPQIKVNLNY 56

Qy 61 RGTGASQDPDNRFDRLFNASRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120

Db 57 RKGLPQSDPDRFDRLFSVSRGVPEELTGLLEYLRTSKYLTDSEYTGSTGKTCL 116

Qy 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAQCTDDYIRGHSALHIAIEKRSLSQCVK 180

Db 117 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAQCTDEFYRHSALHIAIEKRSLSQCVK 176

Qy 181 LLVENGANVHARACGRFFQKQGTCTFYFGEPLPLSLAACTKQWDVSYLLENPHOPASLOA 240

Db 177 LLVENGANVHARACGRFFQKQGTCTFYFGEPLPLSLAACTKQWDVSYLLENPHOPASLEA 236

Qy 241 TDSQGNVTVLHALVMI SDNSAENALTVMYDGLLOAGARLCPTVQLEDIRNLDLTPLKL 300

Db 237 TDSLGNVTVLHALVMIADNSPENSALVIMYDLSLQMGARLCPTVQLEDICNHGLTPLKL 236

Qy 301 AAKEGKIEIFRHILOREFSGL-SHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIA 359

Db 297 AAKEGKIEIFRHILOREFSGLYQPLSRKFTWCYGPVRVSLYDLSSVDSWEKNSVLBIIA 356

Qy 360 FHCKSPHRHVMVLEPLNKLLOAKWDLILPKFPLNCLNIYMFIFTAVAYHQTLLKQAA 419

Db 357 FHCKSPHRHVMVLEPLNKLLOAKWDLILPRFFNFACYLVMIIFTIVAYHQSLEQPA 416

Qy 420 APHLKAEGVNSMLTGHILILGGLIYLLVGLQWYFWRHVFIIWISFIDSYFEILFLFOAL 479

Db 417 IPSSKATFGDSMLLGHILILGGLIYLLVGLQWYFWRHVFIIWISFIDSYFEILFLFOAL 476

Qy 480 LTWVSQVLCFLAIEWILPLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRDLRLFL 539

Db 477 LTWLSQVLPFVETEWYLPVLSVSLVGLWNLNLYYTRGFQHTGIYSVMIQVILRDLRLFL 536

Qy 540 LIYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEGDEGNGAQYRGILEASLE 599

Db 537 LVYLVFLFGFAVALVSLSREARSPKAPENSTTVTEKPTLGQEE--PVPYGILDLASLE 594

Qy 600 LKFTTIGMELAFQELHFRGMVLLLLAYVLLTYLILNMLIALMSETVNSVATDSWSI 659

Db 595 LKFTTIGMELAFQELHFRGMVLLLLAYVLLTYLILNMLIALMSETVNSVATDSWSI 654

Qy 660 WKLOKAI SVLEMENGYWCRKKQ-RAGVMLTVGTGPDGSDPDRWCFRVEEVNWSAEQTL 718

Db 655 WKLOKAI SVLEMENGYWCRKKRHRAGRLKVGTGKDGIDPDRWCFRVEEVNWSAEQTL 714

Qy 719 PTLCEDPSGAGVPTLENVPLASPKEDBDGASEENYVPVQLQSN 764

Db 715 PTLSEDPGAGITGYKKNPT----SKPGKNSASEEDHLPQLVQLQSH 756

RESULT 4

Q6JGX2 PRELIMINARY; PRT; 756 AA.
 ID Q6JGX2

```
AC O6JGX2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TRPV2 protein.
OS F-11 rat/mouse fusion cell line.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
OC mouse/rat hybrid cell lines.
OX NCBI_TaxID=266798;
RN [1]
RP SEQUENCE FROM N.A.
RA Bender F., Mederos y Schnitzler M. V, Li Y., Ji A., Weihe E.,
RA Gudermann T., Schaefer M.K.H.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY487844; AAS66752.1; -.
DR GO; GO:001021; C:integral to membrane; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR Pfam; PF00023; Ank; 3.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR SMART; SM00248; ANK; 4.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR KW ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ SSSEQUENCE 756 AA; 85965 MW; C0E537AB2C96E1A8 CRC64;

Query Match 78.9%; Score 3158; DB 2; Length 756;
Best Local Similarity 80.3%; Pred. No. 2.9e-215;
Matches 615; Conservative 55; Mismatches 84; Indels 12; Gaps 5;

QY 1 MTSPPSPVRLFTLDGQDGSADRGKLDGSGLPMPESQPGEDRKFAQIRVNLNY 60
DB 1 MTSASNPAPARLTSDGDEGSAEVNKGK---NEPPMPESPQGEDRNFSPQIKVNLNY 56
QY 61 RKTGASQDPNPFDRDLFNAVSRGVPEDLAGLPEYLSKSTKYLTDSTYEGSTGKTCL 120
DB 57 RKGGLGPSQDPNPFDRDLFNVSVSRGVPPELTGLLEYLRRTSKYLTDSAYTEGSTGKTCL 116
QY 121 MKAVLMDQGVNACILPLQIDRDSGNPQPLVNAQCTDDYVRGHSALHIAIEKRSIQCVK 180
DB 117 MKAVLMDQGVNACILPLQIDRDSGNPQPLVNAQCTDEYVRGHSALHIAIEKRSIWCVK 176
QY 181 LLVENGANVHARACGRFFQKQGQCTCFYFGLPLSLAACTQMDVSVYLLNPHQPSLAQ 240
DB 177 LLVENGANVHARACGRFFQKQGQCTCFYFGLPLSLAACTQMDVSVYLLNPHQPSLEA 236
QY 241 TDSQGVTLHALVMIISDENSEALVTSMYDGLLOAGARLCPTVQLEDINLQDLTPKL 300
DB 237 TDSLGNVTLHALVMIADNSPENSALVTSMYDGLLOAGARLCPTVQLEDICNHQGLTPKL 296
QY 301 AAEGEKIEIPRHILQREFSGI-SHLGRKFTWCYGPVRVSLYDASVDSCEENSVEIITA 359
DB 297 AAEGEKIEIPRHILQREFSGLYQLSRKFTWCYGPVRVSLYDSSVDSWEKNSVLEIITA 356
QY 360 FHCKSPHRHVMVLEPLNKLQAKWDLIIKPKFLNLCNLIYMFITAVAYHQPOTLKQA 419
DB 357 FHCKSPHRHVMVLEPLNKLQEKWDLIIPRFFNFACVLYVMIIFTIVAYHQPSEQA 416
QY 420 APLKBAVGNMMLTGHIILLGGIYLLVQCLMYFWRHVPFIWISIDSFFELFLFOAL 479
DB 417 IPSKSAFTGDSMLLGHILLGGIYLLVQCLMYFWRHVPFIWISIDSFFELFLFOAL 476
QY 480 LTVVSVOLCFIAIEWYLPLVSLVSLVGLWNLNLYYTRGFQHTGIYSYVMIQKVLRLDLREL 539
DB 479 LTVVSVOLCFIAIEWYLPLVSLVSLVGLWNLNLYYTRGFQHTGIYSYVMIQKVLRLDLREL 536
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DB 477 LTVLSQVLRFEVETEWYLPVSSLVGLWNLNLYYTRGFQHTGIYSYVMIQKVLRLDLREL 536
QY 540 LIYLVFLFGPAVALVSLSOEAWRPEAPGPNATSVSQPMGEQEDRGNAQYRGILEASLE 599
DB 537 LVYLVFLFGPAVALVSLSRAPSDSNTPTEKPTLQGESE--PVPYGGILDASLE 594
QY 600 LFKFTIGMGLAFQBLHFRGMVLLLLAYVLLTVLLLNMLIALMSETVNSVATDSWSI 659
DB 595 LFKFTIGMGLAFQBLHFRGMVLLLLAYVLLTVLLLNMLIALMSETVNSVATDSWSI 654
QY 660 WKLOKAIISVLEMEYNGYWMCRKKQ-RAGVMLTVGTGKPDGSPDERWCFRVEEVNNAWSEOTL 718
DB 655 WKLOKAIISVLEMEYNGYWMCRKRHRAGRLIKVGTGKDGIPDERWCFRVEEVNNAWSEOTL 714
QY 719 PTLCEDPGAGVPTLLENPLVSLASPKPEDEGASEENYVPVQLQSN 764
DB 715 PTLSEDPGAGVPTLLENPLVSLASPKPEDEGASEENYVPVQLQSN 756

RESULT 5
Q99K71
ID Q99K71 PRELIMINARY; PRT; 756 AA.
AC Q99K71;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Trpv2 protein (Mus musculus 2 days neonate thymus thymic cells cDNA,
DE RIKEN full-length enriched library, clone:E430035F12 product:vanilloid
DE receptor-like protein 1, full insert sequence).
GN Name=Trpv2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmitz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
```

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [5]
 RN SEQUENCE FROM N.A.
 RP STRAIN=NOD; TISSUE=Thymus;
 RC The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 [6]
 RN SEQUENCE FROM N.A.
 RP STRAIN=NOD; TISSUE=Thymus;
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RX Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RN SEQUENCE FROM N.A.
 RP STRAIN=NOD; TISSUE=Thymus;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Carninci P., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RN SEQUENCE FROM N.A.
 RP STRAIN=NOD; TISSUE=Thymus;
 RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005415; AA05415.1; -;
 DR EMBL; AK089004; BAC0695.1; -;
 DR MGD; MGI:1341836; Trpv2.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR GO; GO:0005261; P:cation channel activity; IDA.
 DR GO; GO:0009286; P:response to temperature; IDA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR004729; TrpChannel.
 DR InterPro; IPR008347; Vanil_receptor.
 DR Pfam; PF00023; Ank; 4.
 DR Pfam; PF00520; Ion trans; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR01768; TRPVRECEPTOR.
 DR SMART; SM00248; ANK; 4.
 DR TIGRPFAMs; TIGR00870; trp; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 1.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
 KW Transport.
 SQ SEQUENCE 756 AA; 85965 MW; C0B537AB3C86E1A8 CRC64;

Query Match 78.9%; Score 3158; DB 2; Length 756;
 Best Local Similarity 80.3%; Pred. No. 2.9e-215;
 Matches 615; Conservative 55; Mismatches 84; Indels 12; Gaps 5;
 QY 1 MTPSSSPVFRLETLDDGGQDGEADRGKLDGSGLPMPMESQFQGEDRKFAPQIRVNLNY 60
 DB 1 MTSASNPPAPRLTSDGDEGSAEYVNGK-----NEPPPMESPFQGEDRNFSPQIKVNLNY 56
 QY 61 RKGTCASQDPNRFDRDLFNAVSRGVPRDLAGLPEYLSKTSKYLTDSTYTGSTGKTCL 120
 DB 57 RAGLGPQQDPNRFDRDLFNVSRGVPRDLGLLELARTSKYLTSDSTYTGSTGKTCL 116
 QY 121 MKAVLNLDKGVNACILPLQLIDRDSGNPQPLVNAOCTDDYTRGHSAHIAIEKRSLOCVK 180
 DB 117 MKAVLNLDKGVNACILPLQLIDRDSGNPQPLVNAOCTDFYRSHSAHIAIEKRSLSWCVK 176
 QY 181 LLVENGANVHARACGPFQKQGTCTYFGEPLSLSLAACTKQWDVSVLLLENPHOPASLOA 240
 DB 177 LLVENGANVHARACGPFQKQGTCTYFGEPLSLSLAACTKQWDVSVLLLENPHOPASLEA 236
 QY 241 TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLLOAGARLCPTVQLEDIRNLQDLTPLKL 300
 DB 237 TDSLGNVTLHALVMIADNSPENSALVIHMYDSLLOAGARLCPTVQLEDICNHQGLTPLKL 296
 QY 301 AAKEGKIEIFRHILQREFSGL-SHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIA 359
 DB 297 AAKEGKIEIFRHILQREFSGLYQPLSRKFTWCYGPVRVSLYDLSSVDSWEKNSVLEIIA 356
 QY 360 FHCKSPHRHMVLEPLNKLQAKWDLPLPKPLNLCNLIYMFITAVAYHQTPLKQOA 419
 DB 357 FHCKSPHRHMVLEPLNKLQEKNDRLIPRFFNFACLYVYMLIIFTIVAIHQPSLEQPA 416
 QY 420 APHLKAEVGNMLLTGHILLIGIYLLVQGLWYFWRHVFIIWISFIDSYFEILFLFOAL 479
 DB 417 IPSSKATFGDSMLLGHILLIGIYLLVQGLWYFWRHVFIIWISFIDSYFEILFLFOAL 476
 QY 480 LTVVSVQLCFLAIEWYLPLLVLSALVGLWNLVLLLYYTRGFQHTGTIYSVMIQVILRDLRFL 539
 DB 477 LTVVSVQLCFVETEWYLPVLLVSSVLGWLNLVLLYYTRGFQHTGTIYSVMIQVILRDLRFL 536
 QY 540 LIYLVLFQFAVALVSLSQEAWRPEAPTGNATESVQPMGEQDEGNGAQRGILEASLE 599
 DB 537 LVTVLVLFQFAVALVSLSREARSPKPEDSNITVTTEKPTLGQEE--PVPYGGILDASLE 594
 QY 600 LPKFTTIGMGLAFQEOQLHPRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSI 659
 DB 595 LPKFTTIGMGLAFQEQRLFRGVVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSI 654
 QY 660 WKLQKAI SVLEMENGYWCCRKKQ-RAGVMLTVGTPDGSPPDERWCPRVEEVNNAWSQTL 718
 DB 655 WKLQKAI SVLEMENGYWCCRKRHRAGRLKVGTKDGI PDERWCPRVEEVNNAWAEKTL 714
 QY 719 PTLCEPDPGAGVPRTELENPVLASPPKDEDEGASEENVVYVQLQSN 764
 DB 715 PTLSEDPGAGITGYKKNPT----SKPGKNSASEEDHLPLQVLOSH 756

RESULT 6

Q9WUD2 PRELIMINARY; PRT; 761 AA.
 AC Q9WUD2;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Vanilloid receptor-like protein 1.
 GN Name=VRL-1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OK NCBI_taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.


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RC STRAIN=Sprague-Dawley;
RX MEDLINE=99215558; PubMed=10201375; DOI=10.1038/18906;
RA Caterina M.J., Rosen T.A., Tominaga M., Brake A.J., Julius D.;
RT "A capsaicin-receptor homologue with a high threshold for noxious
RL heat.";
RL Nature 398:436-441(1999).
DR EMBL; AF129113; AAD26364.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR004729; TRPChannel.
DR Pfam; PF00023; Ank; 4.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 4.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 761 AA; 86689 MW; 46A281183EBE672F CRC64;

Query Match 76.2%; Score 3051.5; DB 2; Length 761;
Best Local Similarity 77.7%; Pred. No. 1e-207;
Matches 598; Conservative 62; Mismatches 93; Indels 17; Gaps 7;

Qy 1 MTSPPSSPVFRLETLDGQEDSGEADRGKLD FGSGLPPMESQFGEDRKFAQIRVNLNY 60
Db 1 MTSASSPPAFRLTSDGDEGNAEVNKGQE----PPPMESPFQREDRNSSPQIKVNLNF 56
Qy 61 ----RKGTA-SQDPNRPDRDLFNASRGVPEDLAGLP EYLSTKYLTDSEYTEGST 115
Db 57 IKRPKNKTSAPSQEPDRDRDLFSVSRGVPPELTGLLE YLRWNSKYLTDSEYTEGST 116
Qy 116 GKTCLMKAVLNLDGQVNAACILPLLOIDRDSGNPQPLVNAOCTDDYVRGHSALHIAIEKRS 175
Db 117 GKTCLMKAVLNLDGQVNAACIMPLLOIDKDSGNPKLLVNAOCTDEFYQGHSAHIAIEKRS 176
Qy 176 LQCVKLLVNGANVHARACGRFFQKGQGTCTFYFGE LPLSLAACTKQWDVVSVLLENPHQ 235
Db 177 LQCVKLLVNGADVHLRACGRFFQKHQGTCTFYFGE LPLSLAACTKQWDVVVYLLLENPHQ 236
Qy 236 ASLQATDSQGNTVLHALVMSIDNSAENIALVTSMDGL LQAGARLCTPTVQLSDIRNLQDL 295
Db 237 ASLEATDSLGNTVLHALVMIADNSPENSALVIHMYDGL LQMGARLCTPTVQLEBISNHQGL 296
Qy 296 TPLKLAKEGKIIFRHILQREFSG-LSHLSRKFTWCYGPVRVSLYDLASVDSCBENS 354
Db 297 TPLKLAKEGKIIFRHILQREFSGPQPLSRKFTWCYGPVRVSLYDLSSVDSEKNSV 356
Qy 355 LEIIAFHCKSPHRHVMVLEBPLNKLQAKWDLLIPKFF LNLNLYMFTFVAVAHQPT 414
Db 357 LEIIAFHCKSPHRHVMVLEBPLNKLQEKWDRLVSRFF FNFCYLVYMFIFTVAVYHQS 416
Qy 415 LKQAPHLKAEVGNMGLTGHIILLGGIYLLVGLWYFWR RHVFTWISFIDSYEILF 474
Db 417 LDQAPLPSKATFGESMLLGHILILLGGIYLLGQLWYFWR RLFTWISFMDSEYILF 476
Qy 475 LFOALLTVSVQVLCFLAIEWYLPVLSLVGLWNLNLYYTR GFQHTGIYSVMVQKVLIRD 534
Db 477 LFOALLTVLSQVLRPFMETEWYLPVLSLVGLWNLNLYYTR GFQHTGIYSVMVQKVLIRD 536
Qy 535 LLRFLLIYVFLFGFAVALVSLSOEAWRPAEPTGPNAT ESVPQMEQDEGNGAQVRGIL 594
Db 537 LLRFLLIYVFLFGFAVALVSLREARSAPRADNNSVTVE QPTVGOEEB--PAPYRSIL 594
Qy 595 EASLELFKFTIGMGELAFQGLFRGVNLLLLAYVLLTY LLLNMLIALMSETVNSVAT 654
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Db 595 DASLELFKFTIGMGELAFQGLFRGVNLLLLAYVLLTY LLLNMLIALMSETVNSVAT 654
Qy 655 DSWSIWKLOKAIISVLEMENGYWYC-RKKQACAGVMTU VTGPKDGPDPERWCFRVEEYNWAS 713
Db 655 NWSIWKLOKAIISVLEMENGYWYCRRKKHREGRLLLKV GTRGDTDERWCFRVEEYNWAA 714
Qy 714 WEQTLPTLCEDSGAGVPRTLNPLVLPSPKDEDEGAS EENYVPVQLLOS 763
Db 715 WEKTLPTLSEDPSPGFTGNKNPT-----SKPGKNSA SEEDHLPLQVLQS 760

RESULT 7
Q9QYH8 PRELIMINARY; PRT; 761 AA.
ID AC Q9QYH8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stretch activated channel 2b.
GN Name-rSAC2b;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishibashi K.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029330; BAA89637.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR008347; Vanil_receptor.
DR Pfam; PF00023; Ank; 4.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR SMART; SM00248; ANK; 4.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 761 AA; 86705 MW; 8977CDB1D5351EC8 CRC64;

Query Match 76.0%; Score 3041.5; DB 2; Length 761;
Best Local Similarity 77.5%; Pred. No. 5.3e-207;
Matches 597; Conservative 62; Mismatches 94; Indels 17; Gaps 7;

Qy 1 MTSPPSSPVFRLETLDGQEDSGEADRGKLD FGSGLPPMESQFGEDRKFAQIRVNLNY 60
Db 1 MTSASSPPAFRLTSDGDEGNAEVNKGQE----PPPMESPFQREDRNSSPQIKVNLNF 56
Qy 61 ----RKGTA-SQDPNRPDRDLFNASRGVPEDLAGLP EYLSTKYLTDSEYTEGST 115
Db 57 IKRPKNKTSAPSQEPDRDRDLFSVSRGVPPELTGLLE YLRWNSKYLTDSEYTEGST 116
Qy 116 GKTCLMKAVLNLDGQVNAACILPLLOIDRDSGNPQPLVNAOCTDDYVRGHSALHIAIEKRS 175
Db 117 GKTCLMKAVLNLDGQVNAACIMPLLOIDKDSGNPKLLVNAOCTDEFYQGHSAHIAIEKRS 176
Qy 176 LQCVKLLVNGANVHARACGRFFQKGQGTCTFYFGE LPLSLAACTKQWDVVSVLLENPHQ 235
Db 177 LQCVKLLVNGADVHLRACGRFFQKHQGTCTFYFGE LPLSLAACTKQWDVVVYLLLENPHQ 236
Qy 236 ASLQATDSQGNTVLHALVMSIDNSAENIALVTSMDGL LQAGARLCTPTVQLSDIRNLQDL 295
Db 237 ASLEATDSLGNTVLHALVMIADNSPENSALVIHMYDGL LQMGARLCTPTVQLEBISNHQGL 296
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QY 296 TPLKLAKEGKIEIFRHILQREFSG--LSHLSRKFTWCYGPVRVSLYDLASVDSCEANSV 354
DB 297 TPLKLAKEGKIEIFRHILQREFSGPYQPLSRKFTWCYGPVRVSLYDLSSVDSWEKNSV 356
QY 355 LEIIAFHCKSPHRRMVVLEPLNKLQAKWDLILPKFFLNFCLNLIYMFIFTAVAYHQT 414
DB 357 LEIIAFHCKSPHRRMVVLEPLNKLQAKWDLVSRFFNFACLYVMFIFTVAYHQS 416
QY 415 LKQQAAPHLKAEVGNMMLTGHLILLLGGIYLLVGLWYFWRHVPFIWISFSDSYEILF 474
DB 417 LDQALPSSKATPGESMMLLGHILLLGGIYLLVGLWYFWRHVPFIWISFSDSYEILF 476
QY 475 LFOALLTVVSQVLCFLAIEWYLLVLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRD 534
DB 477 LQALLTVLSQVLRFMETEWYLLVLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRD 536
QY 535 LRLFLIYLVFLFGFAVALVLSQZAWRPEAPTGPNNATESVQPMQEGDEGNGAQYRGIL 594
DB 537 LRLFLIYLVFLFGFAVALVLSRREARSPPKEDNNSTVTQPTVQGBEE--PAPYRSIL 594
QY 595 EASLELFPKFTIGMGLAFQELFRGVMVLLLLAYVLLTYVLLLNLMALMSETVNSVAT 654
DB 595 DASLELFPKFTIGMGLAFQELFRGVMVLLLLAYVLLTYVLLLNLMALMSETVNSVAD 654
QY 655 DWSIWKLOKAI SVLEMENGYWMC--RKKQAGVMLTVGTPDGSPPDERWCFCRVEEVNWA 713
DB 655 NWSIWKLOKAI SVLEMENGYWMCRRKKHREGKLLKVGTRGDTGTPDERWCFCRVEEVNWA 714
QY 714 WEOTLPTLCEDPGAGVPRTPLENPVLASPPKEDGASBENYVPVQL 763
DB 715 WEKTLPTLSEDPGPGITGNKNPT----SKPGKNSASBEDHLPLOVLOS 760

RESULT 8
Q9JM18 PRELIMINARY; PRT; 762 AA.
AC Q9JM18;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Ion channel.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Suzuki M.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB022332; BAA93435.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion_Crims.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR Pfam; PF00023; Ank; 4.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR SMART; SM00248; ANK; 4.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 762 AA; 86767 MW; C80970BC4195351E CRC64;

Query Match 75.6%; Score 3028.5; DB 2; Length 762;
Best Local Similarity 77.4%; Pred. No. 4.5e-206;
Matches 594; Conservative .62; Mismatches 94; Indels 17; Gaps 7;
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QY 1 MTSPPSSPVFRLETLTGGQEDGSEADRGKLDGSGLPMMESQFQGEDRKFAFQIRVNLAY 60
DB 1 MTSASSPPAFRLTSDGDEGNAEVNKGQOE---PPMESPFQEDRNSSPQIKVNLNF 56
QY 61 ----RKGTCG--SQDPNPRFDRRLFNARSRGVPEDLAGLPEYLSKTSKYLTDSEYEGST 115
DB 57 IKRPKNTSAPSQSBPDRDLFSVVSRRGVPBELTGLLEYLRWNSKYLTDSEYEGST 116
QY 116 GKTCLMKAVNLKQGNACILPLLOIDRDSGNPQPLVNAQCTDDVYRGHSALHIAIEKRS 175
DB 117 GKTCLMKAVNLKQGNACIMPELLQIDKDSGNPKLLVNAQCTDEFPQGSALHIAIEKRS 176
QY 176 LQCVKLLVNGANVHARACGRFFQKQGTCTFFYFGLPLSLAACTQKQWVSVYLLNPHQP 235
DB 177 LQCVKLLVNGADVHLRACGRFFQKQGTCTFFYFGLPLSLAACTQKQWVSVYLLNPHQP 236
QY 236 ASLQATDSQNTVHALVMSIDNSAENALVTSMVDGLLQAGARLCPTVOLEDIRNLQDL 295
DB 237 ASLEATDSLGNTVLHALVMIADNSPENSALVTHTMDGLLQMGARLCPTVOLEISNHQGL 296
QY 296 TPLKLAKEGKIEIFRHILQREFSG--LSHLSRKFTWCYGPVRVSLYDLASVDSCEANSV 354
DB 297 TPLKLAKEGKIEIFRHILQREFSGPYQPLSRKFTWCYGPVRVSLYDLSSVDSWEKNSV 356
QY 355 LEIIAFHCKSPHRRMVVLEPLNKLQAKWDLILPKFFLNFCLNLIYMFIFTAVAYHQT 414
DB 357 LEIIAFHCKSPHRRMVVLEPLNKLQAKWDLVSRFFNFACLYVMFIFTVAYHQS 416
QY 415 LKQQAAPHLKAEVGNMMLTGHLILLLGGIYLLVGLWYFWRHVPFIWISFSDSYEILF 474
DB 417 LDQALPSSKATPGESMMLLGHILLLGGIYLLVGLWYFWRHVPFIWISFSDSYEILF 476
QY 475 LFOALLTVVSQVLCFLAIEWYLLVLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRD 534
DB 477 LQALLTVLSQVLRFMETEWYLLVLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRD 536
QY 535 LRLFLIYLVFLFGFAVALVLSQZAWRPEAPTGPNNATESVQPMQEGDEGNGAQYRGIL 594
DB 537 LRLFLIYLVFLFGFAVALVLSRREARSPPKEDNNSTVTQPTVQGBEE--PAPYRSIL 594
QY 595 EASLELFPKFTIGMGLAFQELFRGVMVLLLLAYVLLTYVLLLNLMALMSETVNSVAT 654
DB 595 DASLELFPKFTIGMGLAFQELFRGVMVLLLLAYVLLTYVLLLNLMALMSETVNSVAD 654
QY 655 DWSIWKLOKAI SVLEMENGYWMC--RKKQAGVMLTVGTPDGSPPDERWCFCRVEEVNWA 713
DB 655 NWSIWKLOKAI SVLEMENGYWMCRRKKHREGKLLKVGTRGDTGTPDERWCFCRVEEVNWA 714
QY 714 WEOTLPTLCEDPGAGVPRTPLENPVLASPPKEDGASBENYVPVQL 760
DB 715 WEKTLPTLSEDPGPGITGNKNPT----SKPGKNSASBEDHLPLOV 757
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RESULT 9

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Q8QFN9 PRELIMINARY; PRT; 843 AA.
AC Q8QFN9;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Vanilloid receptor-like protein.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dorsal root ganglia;
RX MEDLINE=21842900; PubMed=11853675; DOI=10.1016/S0092-8674(02)00637-2;
RA Jordt S.E., Julius D.;
RT "Molecular basis for species-specific sensitivity to 'hot' chili
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RT Cell 108:421-430(2002).
RL EMBL; A072909; AAL78069.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR InterPro; IPR008348; Vanil_receptor2.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR PRINTS; PR01769; VRL2RECEPTOR.
DR SMART; SM00248; ANK; 4.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 843 AA; 96520 MW; ABB3592C9DC179C8 CRC64;

Query Match 42.3%; Score 1694; DB 2; Length 843;
Best Local Similarity 47.4%; Pred. No. 2.4e-111;
Matches 359; Conservative 118; Mismatches 217; Indels 64; Gaps 12;

QY 4 PSSSPVRLTLDGGQDSEADRGK-----DFGSLPPMESQFGEDRKFAPQ-IRVNLN 59
DB 49 PSKSNIF-----ARRGRFVMGDCDKMAPMDSFYQ-MDHLMAFSPVKFHDN 93
QY 60 YRKG-----TGASQPDNRRDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTD 108
DB 94 MERGKLHLKLLSTDSITGCSSEKAFKYDRRRIFDAVARGSTKLDLDDLLYLNRLKHLTD 153
QY 109 EYEGSTGKTKLMKAVLNKDGVNACILPLQLQIDRDSGNPQPLVNAQCTDDYRGHSA 168
DB 154 EPEKETGKTKLLKMLNLDHGKNDIPLLLDIAGKTGLKPEVNAEYDNTYKGTALH 213
QY 169 IATEKSLQCVKLLVNGANVHARACGRFQKQG--TCFYFGLPLSLAACTQKQWVVSY 227
DB 214 IAIERENMVLKLVQNGADVHARACGEFFRKIKGPKGFYFGLPLSLAACTNQLCIVR 273
QY 228 LLENPHQASLQATDSQNTVLHALYMI SDNSAENIALVTSMDYDGLLQAGARLCPTV 287
DB 274 LLENPYQADIAAEDSGMNVHLTLVEIADNTKNTKFTKMYNNLILQAKINPIKLE 333
QY 288 DIRNLQDLTPKLAKEGKIEIFRHILQREFSG--LSHLSRKFTWCYGPVRVSLYDLAS 345
DB 334 ELTNKGLTPLTAAKTGKIGIFAYILRREIKDPECHLSRKFTWAYGVPVHSSLYDLC 393
QY 346 VDCSENVLEIIATFACKSPHRHMVLEPLNKLQAKWDLIIPK-PFLNLCNLIMFI 404
DB 394 IDTCENSVLEIIAYSSETSRHEMLLVEPLNRLQDKWDRFVKHLFYFNFFFYAIIHSI 453
QY 405 FTAVAHQPTLKQAAAPH-LKAEVGSMLLTGHILILGGIYLLVQLWYFWRHVFWI 463
DB 454 LTAAAYRYPQKGDKPPFAGHGTGEYFRTVGTBLSVLGGLYFFFGIQTFFVRRSLKT 513
QY 464 SFIDSFEIILFLQALITVVSQVLCFLAIEWYLPLLVSAVLGWLNLYYTRGFQHTGY 523
DB 514 LIVDSYSEVILFFVHSLLSLVLYFCGQELYASNVFSLALCWANWLYYTRGFQMGIV 573
QY 524 SVMQKVLRLDLRLFLIYLVLFPGFAVALVSLSQEAMRPEATGPNATESVOPMEGQED 583
DB 574 SVMIAKMLRLDLRCRFVFLVFLFGFSTAVTLLIED-----DNEGQDT 616
QY 584 EGN-----GAQYRGILEASLELPKFTIGMGELAFQEQHLFRGMVLLILLAYVLL 632
DB 617 NSSEYARCSHTKGRTSYNSLYTCLFELPKFTIGMGDLEFTENYRFSKVFLLVLYVIL 676
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QY 633 TYILLNMLIALMSETVNSVATDSWSIWKLQKALSIVLEMENGYWC-RKKQAGWMLTVG 691
DB 677 TYILLNMLIALMGETSVKIAQESKSIWKLQRAITILDINSYLNCLRRSPFSGRVLVG 736
QY 692 TKPGDSPERWCFRVEVNVASWEOQLPTLCEDPGAG 729
DB 737 ITPDQDDYRWCFRVDEVNWSWTNLTNLGINEDPGCSG 774

RESULT 10
O35433 PRELIMINARY; PRT; 838 AA.
AC O35433;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Vanilloid receptor subtype 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX SEQUENCE FROM N.A.
RY MEDLINE=98007969; PubMed=9349813; DOI=10.1038/39807;
RA Caterina M.J., Schumacher M.A., Tominaga M., Rosen T.A., Levine J.D.,
RT Julius D.;
RT "The capsaicin receptor: a heat-activated ion channel in the pain
RT pathway.";
RL Nature 389:816-824(1997).
DR EMBL; AF029310; AAC53398.1; -.
DR PIR; T09054; T09054.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR004729; TRPChannel.
DR InterPro; IPR008347; Vanil_receptor.
DR Pfam; PF00023; Ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR01768; TRPVRECEPTOR.
DR SMART; SM00248; ANK; 4.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
KW Transport.
SQ SEQUENCE 838 AA; 94947 MW; DAF80B12BDF71BF CRC64;

Query Match 41.3%; Score 1652; DB 2; Length 838;
Best Local Similarity 46.3%; Pred. No. 2.3e-108;
Matches 359; Conservative 127; Mismatches 230; Indels 60; Gaps 15;

QY 18 GOEDSEADRGKLDGSGLPFPMESQFGEDRKFAPQIRVN---LNYRKGTG----- 65
DB 51 GKGDSEAS-----PLDCPYEGGLASCPIITVSSVLTITQPCDGPASVRPSQ 99
QY 66 ----ASQDPDNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGKTC 121
DB 100 DSVSAGEKPPRLYDRRSIFDAVAQNCQELSLPLPQSKRLTDSFDPETGKTC 159
QY 122 KAVNLKQGVNACILPLQLQIDRDSGNPQPLVNAQCTDDYRGHSAHIAIKRSLQCVK 181
DB 160 KAWLNHNGQNTIALLLDVARKTUSLKQFVNASTYDSYKGTALHIAERNMTLV 219
QY 182 LVENGANVHARACGRFFQKQG--TCFYFGLPLSLAACTQKQWVVSYLLENPHQAS 240
DB 220 LVENGADVQAAANGDPFFKTKGRPGFYFGLPLSLAACTNQLAIVKFLQNSWQPAD 279
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QY 90 DLGLPEYLSKSYLTDSYEGSTGKCLMKAVLNKDGYNACTLPLQLIDRSGNPO 149
 DB 130 DLDSLLPFLQSKKRTUTDFKDPETGKCLLKAMLNHNQNDITLSLLDARQNSLK 189
 QY 150 PLVNAOCTDDYRGHSAHIAIEKRSLOCVKLLIVENGANVHARACRPFQKQG-TCFYF 208
 DB 190 EFNASYTDSYRGQTALHAIERRNNVLTLLVENGADVQAAANGDFPKTKRPGFYF 249
 QY 209 GELPLSLAACTQKQWVVSYLLENPHOPASLOATDSQGNVTVLHVMISNSAENALVTS 268
 DB 250 GELPLSLAACTQKQWVVSYLLENPHOPASLOATDSQGNVTVLHVMISNSAENALVTS 309
 QY 269 MYDGLLOAGARLCTVQLEDIRNLQDLTPLKAAKGGKIEIPHHILOREP--SGLSHLR 326
 DB 310 MYNEILITLGAKYPTLKLBELTNKGTPLALAASSGKIGVLAIILOREIPEPECHLSR 369
 QY 327 KPTWCYGPVVRVSLYDLASVDSCEENSVEIIAF-HCKSPHRRHVMVLEPLNKLLOAKWD 385
 DB 370 KFTWAYGPHVSSLYDLSCIDTCEKNSVLEVIAYSSETPNRHDMLLVEPLNRLQDKWD 429
 QY 386 LLIPK-FFNLFLCNLYMFIPTAVAYHQPTLKKQAP--HLKAEVGNMMLTGHILILG 442
 DB 430 RFVKRIFYFNFFIYCLYMIIFTMAAYRPV---DGLPPYKQKNTVGDYFRVVTGEILSVIG 486
 QY 443 GIYLLVQOLWYFWRHVFVWISFIDSYFETLPLFQALLTVVSOVLCLALEWVLPLLVSA 502
 DB 487 GFHFFFRGIIQYFLQRRPSVKTLFVDSYSELFFVQSLFLASVVLVFSHRKKEVACWVFS 546
 QY 503 LVLGMLNLYYTRGFQHTGYSYVMIQVILRDLRLFLIYLVFLFQFAVALVLSQEAWR 562
 DB 547 LALGWTNMLYTRGFQMGYIYVMIKMIILDLRCRPMFYVLVFLFGFSTAVVTLIED--- 603
 QY 563 PEAPTEGNATESVQPMQEGDEGNGAQ-----YRGILEASLELFPKFTTGMGELAFQOLH 617
 DB 604 -----GNESLSABPHRW---GPGCRSAKNSYSLYSTCLELFPKFTTGMGDELEFNYD 655
 QY 618 FRGMVLLIYLLAYVLTIVILLNMLIALMSETVNSVATDSWSIKLOKAIASVLEWENGYYW 677
 DB 656 FKAVFIILLAYVLTIVILLNMLIALMGETVNSVATDSWSIKLOKAIASVLEWENGYYW 715
 QY 678 C-RKKORAGVMLTVGTGKPSDBRCFRVEEVNWSAQETLPTLCEDDPSGA-GVPRITL 735
 DB 716 CMKAFRSGLKLVGYTPDGKDDYRCFRVDEVNWTNTNVTNGIINEDPGNCEGVKRTLS 775
 QY 736 NPVLASPPKEDGASEENVVYVOLLQ 762
 DB 776 FSLRSQ---RVSGRNKNKFNALVPLR 798

RESULT 14

Q697L1 PRELIMINARY; PRT; 840 AA.
 AC Q697L1
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 GN Transient receptor potential V1.
 GN Name=TRPV1;
 OS Canis familiaris (Dog).
 OC Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Phelps P.T., Anches J.C., Correll C.C.;
 RT "Cloning and Functional Characterization of Dog TRPV1.";
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY568758; AAT71314.1;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0004872; P:receptor activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.

DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat channel_TrpL.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR004729; TRPChannel.
 DR InterPro; IPR008347; vanil_receptor.
 DR Pfam; PF00023; Ank; 3.
 DR Pfam; PF00520; Ion trans; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR01768; TRPVRECEPTOR.
 DR SMART; SM00248; ANK; 4.
 DR TIGRfams; TIGR00870; trp; 1.
 DR PROSITE; PS50088; ANK REPEAT; 1.
 DR PROSITE; PS0297; ANK REP REGION; 1.
 KW ANK repeat; Ion transport; Ionic channel; Receptor; Transmembrane;
 KW Transport.
 SQ SEQUENCE 840 AA; 95236 MW; 5F5D5A366DC46459 CRC64;
 Query Match 41.2%; Score 1649; DB 2; Length 840;
 Best Local Similarity 50.0%; Pred. No. 3,7e-108;
 Matches 340; Conservative 116; Mismatches 208; Indels 16; Gaps 9;
 QY 64 TCASQDPNRPDRDRLENAVSRGVPEDLAQLPEYLSKTSKYLTDSEYTBGSGTKCLMKA 123
 DB 103 TAGSEKSLKYDRRKIFEAVQNCELOSLLFLQSKKHLMDSEFKDPETGKTCLLKA 162
 QY 124 VLNLKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSQCQVKLLV 183
 DB 163 MLNLHDGQNDTPLLLEIARQDLSLKLNASYDTSYKGGQTALHAIERRNNMALVTLV 222
 QY 184 ENGANYHARACRPFQKQG-TCFYFGEPLSLAACTQKQWVVSYLLENPHOPASLOATD 242
 DB 223 ENGADVQAAANGDFPKTKRPGFYFGEPLSLAACTQKQWVVSYLLENPHOPASLOATD 282
 QY 243 SQGNVTVLHVMISNSAENALVTSMYDGLLOAGARLCTVQLEDIRNLQDLTPLKLA 302
 DB 283 SVGNTVHLALVEADNADNTAFVTSYNEILLGAKLHPTLKEGLTKKGLTPLALAA 342
 QY 303 KEGKIEIPHHILOREPS--GLSHLSRKFTWCYGPVVRVSLYDLASVDSCEENSVEIIAF 360
 DB 343 RSGKIGVLAIILOREIPEPECHLSRKFTWAYGPHVSSLYDLSCIDTCEKNSVLEVI 402
 QY 361 -HCKSPHRRHVMVLEPLNKLLOAKWDLIPK-FFNLFLCNLYMFIPTAVAYHQPTLKKQ 418
 DB 403 SSSETPNRHDMLLVEPLNRLQDKWDRFVKRIFYFNFFIYCLYMIIFTMAAYRPV--- 459
 QY 419 AAP--HLKAEVGNMMLTGHILILGIGIYLLVQOLWYFWRHVFVWISFIDSYFELFLF 476
 DB 460 GLPPYKLVKHTVGDYFRVVTGEILSVLGVIYFFRGIIQYFLQRRPSLKTFLVDSYSEMLFFV 519
 QY 477 QALLTVVSOVLCLALEWVLPLLIYLVSAVLSALVGLNLLYYTRGFQHTGYSYVMIQVILRDL 536
 DB 520 QSLFMLGTVVLYFCHHKEYVASVMSVSLANGWTNMLYYTRGFQMGYIYVMIKMIILDL 579
 QY 537 RFLIYLVFLFGFAVALVLSQEAWRPEAPTEGNATESVQPMQEGDEGNGAQVGRGLEA 596
 DB 580 RFMFVYLVLFGFSTAVVTLIEDGKNSVPT-----ESTLHRWRGPGCRPPDSSNSLYST 635
 QY 597 SLELFPKFTTGMGELAFQOLHFRGMVLLIYLLAYVLTIVILLNMLIALMSETVNSVATDS 656
 DB 636 CLELFPKFTTGMGDELEFNYDFKAVFIILLAYVLTIVILLNMLIALMGETVNSVATDS 695
 QY 657 WSKWKLQKAIASVLEWENGYYW-C-RKKORAGVMLTVGTGKPSDBRCFRVEEVNWSAQ 715
 DB 696 KNIWKLOKAIASVLEWENGYYW-C-RKKORAGVMLTVGTGKPSDBRCFRVEEVNWSAQ 755
 QY 716 QTLPTLCEDDPSGA-GVPRITL 734
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 Q9H0G9
 ID Q9H0G9 PRELIMINARY; PRT; 839 AA.

AC Q9H0G9;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2004 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKFp434K0220.
 GN Name=DKFp434K0220;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RG The German cDNA Consortium;
 RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A.,
 RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL136801; CAB66735.1; --
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR004729; TRPChannel.
 DR InterPro; IPR008347; Vanil_receptor.
 DR InterPro; IPR008348; Vanil_receptor2.
 DR Pfam; PF00023; Ank; 3.
 DR Pfam; PF00520; Ion_trans; 1.
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 DR PRINTS; PR01769; VRL2RECEPTOR.
 DR SMART; SM00248; ANK; 4.
 DR TIGRFAMs; TIGR00870; tip; 1.
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 KW ANK repeat; Hypothetical protein; Ion transport; Ionic channel;
 KW Transmembrane; Transport.
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Query Match 41.2%; Score 1648.5; DB 2; Length 839;
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QY 74 FDRRLFNVAISGVGPDLAGLPYLSKTYLTDSEYTGSTGKTCIMKAVLMLKDGVNA 133
 DB 113 YDRRSIFEAVANNQDLESLLFLQSKKHLTDNEFDPECTGKTLKAKMLNLDHGQNT 172

QY 134 CILPLIQIDRDSGNPQPLVNAOCTDDYYRGHSAIHIAIEKRSLOQCVKLLVENGANYHARA 193
 DB 173 TIPLLLEIARQTDLSKELVNASYTDSSYKGQTAHIAIERNNMALVTLLVENGADYQAAA 232

QY 194 CGRFFFOKQOG-TCFYFGEPLSLAACTKQWDVVSYLLENPHOPASLOATDSOGNTVLHAL 252
 DB 233 HGDFFFKTKRGPGFYFGEPLSLAACTNQLGIKVFLLQNSQWQTADISARDSVGNVTVLHAL 292

QY 253 VMISDNSAENIALVTSMDGLQAGARLCPTVOLEDIRNLQDITPLKAAKEGKIEIFRH 312
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QY 313 ILQREPS--GLSHLSRKFTWCYGPVRSVLYDLASVDSCEANSVLEIIAF-HCKSPHRR 369
 DB 353 ILQREIQEPECRHLSRKFTWAYGPPVHSSLYDLSDICTCKNSVLEIAYSSSETPNRHD 412

QY 370 MVVLEPLNKLLOAKWDLIPK-FELNPLCNLIYMFIFTAVAYHOPTLKKQAAAPHLKAE-V 427
 DB 413 MLIVLEPLNRLLOKWDKRFVRIFFNPLVCLYMLIFTMAAYRPV---DGLPPFQWEKI 469

QY 428 GNSMLITGHTLILGGYLLVGLQWYFWRHVPFIWISFIDSYFEILFLFOALLTVVVSQVL 487
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QY 488 CFLAIEWYLLVLSALVGLWNLVLYYTRGFQHTGIYSVMIQKVILRDLLRFLLIYLVFLF 547

DB 530 YFSLHKEYVASVFSALGWTNMLYTRGFQOMGIYAVMIKMLRDLCRFMFVIVFLF 589
 QY 548 GFAVALVSLSQEA-----WRPEAPTGNATESVQPMEGQDEGNGAQYRGIL 594
 DB 590 GFSTAVVTLLIEDGKNDLSLPSESTSHRWGSPACRPPDSS-----YNSLY 632
 QY 595 EASLELPKFTICMGELATQEQHPRGMVLLLLAYVLLTYILLNMLIALMSETVNSVAT 654
 DB 633 STCLELPKFTICMGDLFTENYDFKAVFIILLAYVILTYILLNMLIALMGETVNKIAQ 692
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 DB 693 ESKNIWKQORALITIDTEKSFUKWKAKFRSKGLQVGYTPDGKDDYRCFRVDEVNWT 752
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 DB 753 WNTNVGIINEDPGNCEGVKRTLSFSLRSS----RVSGRHWKNFALVPLLR 798

Search completed: October 5, 2005, 11:20:56
 Job time : 86 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: / October 5, 2005, 11:23:55 ; Search time 167 Seconds
(without alignments)
1899.094 Million cell updates/sec

Title: US-09-445-614B-2
Perfect score: 4004
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4004	100.0	764	9	US-09-828-466-4
2	4004	100.0	764	10	US-09-978-303-36
3	4004	100.0	764	14	US-10-000-823-6
4	4004	100.0	764	15	US-10-342-844-68
5	4004	100.0	764	16	US-10-757-262-26
6	4004	100.0	764	16	US-10-473-127-761
7	4004	100.0	764	16	US-10-473-127-762
8	4004	100.0	764	16	US-10-473-127-765
9	4004	100.0	764	16	US-10-473-127-770
10	4004	100.0	764	16	US-10-473-127-772
11	4004	100.0	764	16	US-10-473-127-776

12	4004	100.0	764	16	US-10-473-127-779
13	4004	100.0	764	17	US-10-915-017-36
14	4004	100.0	764	20	US-11-013-090-5
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16	3998	99.9	764	16	US-10-473-127-766
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20	3988.5	99.6	763	16	US-10-473-127-774
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23	3945	98.5	764	15	US-10-342-844-70
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25	3945	98.5	764	16	US-10-473-127-778
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ALIGNMENTS

RESULT 1
US-09-828-466-4
; Sequence 4, Application US/09828466
; Patent No. US20020035056A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A.J.
; APPLICANT: silos-Santiago, Immaculada
; TITLE OF INVENTION: 54420, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: MNI-125CP
; CURRENT APPLICATION NUMBER: US/09/828,466
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/544,797
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-466-4

Query Match	100.0%;	Score	4004;	DB	9;	Length	764;
Best Local Similarity	100.0%;	Pred. No.	0;				
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Gaps	0;						
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Db	61	RKGTGASQPPNFRDRRLFNASRGVPEDLAGLPEYLSKTYLTDSEYTEGSGTKTCL	120				
Qy	121	MKAVALNLKDGVNACILFLQLIDRDSGNPQPLVNAQCTDDYYRGHSAHLIAIEKRSLOCVK	180				

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Db 181 LLVENGANVHARACGRFFQKGQCTCFYFGELPLSLAACTKQMDVVSYLENPHQPASLOA 240
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Db 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLOAGARLCPTVOLEDIRNLODLPKL 300
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RESULT 2
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; Sequence 36, Application US/09978303
; Publication No. US20030049728A1
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsacin receptor and capsacin receptor-related
; TITLE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-303-36

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 6, Application US/10000823
; Publication No. US20030027164A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING A NC
; TITLE OF INVENTION: HUMAN ION CHANNEL EXPRESSED IN SPINAL CORD AND BRAIN
; FILE REFERENCE: D0109NP
; CURRENT APPLICATION NUMBER: US/10/000,823
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/250,587
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 764

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-823-6

Query Match      100.0%; Score 4004; DB 14; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
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QY 661 KLOKALSVLEMENGYWCRKQKQAGVMLTVGTGKPDGSPDERWCFRVEEVNWSWEQTLPT 720
Db 661 KLOKALSVLEMENGYWCRKQKQAGVMLTVGTGKPDGSPDERWCFRVEEVNWSWEQTLPT 720

QY 721 LCEDPGAGVPRTLENPVLASPPKEDGASEENYVPVQLQSN 764
Db 721 LCEDPGAGVPRTLENPVLASPPKEDGASEENYVPVQLQSN 764
```

```
RESULT 4
US-10-342-844-68
; Sequence 68, Application US/10342844
; Publication No. US20040009537A1
; GENERAL INFORMATION:
; APPLICANT: Roos, Jack
; APPLICANT: Stauderman, Kenneth
; APPLICANT: Velicelebi, G'n I
; TITLE OF INVENTION: METHODS OF MODULATING AND IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT MODULATE INTRACELLULAR CALCIUM
; FILE REFERENCE: 37481-3307
; CURRENT APPLICATION NUMBER: US/10/342,844
```

```
; CURRENT FILING DATE: 2003-01-13
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/347,459
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/401,171
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/405,678
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAD26363
; DATABASE ENTRY DATE: 1999-04-07
; US-10-342-844-68

Query Match      100.0%; Score 4004; DB 15; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPSSPVFRLETLDDGGEDGSEADRGKLDGSGLPMPESQFQGEDRKFAPIQIRVNLNY 60
Db 1 MTSPSSPVFRLETLDDGGEDGSEADRGKLDGSGLPMPESQFQGEDRKFAPIQIRVNLNY 60

QY 61 RGTGASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
Db 61 RGTGASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120

QY 121 MKAVLNKDGVNACILPLLLQIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSIQCVK 180
Db 121 MKAVLNKDGVNACILPLLLQIDRDSGNPQPLVNAOCTDDYRGHSAHIAIEKRSIQCVK 180

QY 181 LLVENGANVHARACGRFFQKGQTCFYFGEPLSLAACTKQWDVSVYLLNPHQASLOA 240
Db 181 LLVENGANVHARACGRFFQKGQTCFYFGEPLSLAACTKQWDVSVYLLNPHQASLOA 240

QY 241 TDSQGNTVLHALVMSDNSAENIALVTSMYDGLQAGARLCTVQLEDIRNLQDLTPLKL 300
Db 241 TDSQGNTVLHALVMSDNSAENIALVTSMYDGLQAGARLCTVQLEDIRNLQDLTPLKL 300

QY 301 AAKEGKIEIFRHIQREFSGLSHRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIAF 360
Db 301 AAKEGKIEIFRHIQREFSGLSHRKFTWCYGPVRVSLYDLASVDSCEENSVLIEIAF 360

QY 361 HCKSPHRHVMVLEPLNKLQAKWDLIIKPFPLNFCNLIYMFIFTAVAYHQTLLKQAA 420
Db 361 HCKSPHRHVMVLEPLNKLQAKWDLIIKPFPLNFCNLIYMFIFTAVAYHQTLLKQAA 420

QY 421 PHLKAEVGNMMLTGHIILGGLYLLVGLQWYFWRHVFVWISFIDSFEILFLQALL 480
Db 421 PHLKAEVGNMMLTGHIILGGLYLLVGLQWYFWRHVFVWISFIDSFEILFLQALL 480

QY 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVLRLDLRFL 540
Db 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVLRLDLRFL 540

QY 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEGDEGNGAQYRGILEASLEL 600
Db 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMQEGDEGNGAQYRGILEASLEL 600

QY 601 FKFTIGMGLAFQEQHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
Db 601 FKFTIGMGLAFQEQHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660

QY 661 KLOKALSVLEMENGYWCRKQKQAGVMLTVGTGKPDGSPDERWCFRVEEVNWSWEQTLPT 720
Db 661 KLOKALSVLEMENGYWCRKQKQAGVMLTVGTGKPDGSPDERWCFRVEEVNWSWEQTLPT 720

QY 721 LCEDPGAGVPRTLENPVLASPPKEDGASEENYVPVQLQSN 764
Db 721 LCEDPGAGVPRTLENPVLASPPKEDGASEENYVPVQLQSN 764
```

```
RESULT 5
US-10-757-262-26
; Sequence 26, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Sillos-Santiago, Inmaculada
; APPLICANT: Eliaaof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MPI03-007PIRNONMIM
; CURRENT APPLICATION NUMBER: US/10757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-757-262-26

Query Match 100.0%; Score 4004; DB 16; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSSPVFRLETLDDGGQEDGSEADRGKLDGSGGLPPMESQFGEDRKFAPQIRVNLNY 60
DB 1 MTSPPSSPVFRLETLDDGGQEDGSEADRGKLDGSGGLPPMESQFGEDRKFAPQIRVNLNY 60
QY 61 RKTGTASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
DB 61 RKTGTASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
QY 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAQCTDDYYRGHSAHIAIEKRSIQCVK 180
DB 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAQCTDDYYRGHSAHIAIEKRSIQCVK 180
QY 181 LIVENGANVHARACGFFQKQGTCTFYFGLPLSLAACCTKQWDVVSYLENPHQPASLOA 240
DB 181 LIVENGANVHARACGFFQKQGTCTFYFGLPLSLAACCTKQWDVVSYLENPHQPASLOA 240
QY 241 TDSQGNVTLHALVMSIDNSAENIALVTSWYDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300
DB 241 TDSQGNVTLHALVMSIDNSAENIALVTSWYDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300

1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
MPI03-007PIRNONMIM
US/10757,262
2004-01-14
US 60/440,318
2003-01-15
US 60/444,783
2003-02-04
US 60/457,901
2003-03-27
US 60/468,775
2003-05-08
US 60/471,614
2003-05-19
US 60/478,742
2003-06-16
US 60/488,529
2003-07-18
US 60/491,156
2003-07-30
US 60/499,594
2003-09-02
US 60/506,332
2003-09-26
136
FastSeq for Windows Version 4.0
26
764
PRT
Homo sapiens

US-10-757-262-26

Query Match 100.0%; Score 4004; DB 16; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSSPVFRLETLDDGGQEDGSEADRGKLDGSGGLPPMESQFGEDRKFAPQIRVNLNY 60
DB 1 MTSPPSSPVFRLETLDDGGQEDGSEADRGKLDGSGGLPPMESQFGEDRKFAPQIRVNLNY 60
QY 61 RKTGTASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
DB 61 RKTGTASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
QY 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAQCTDDYYRGHSAHIAIEKRSIQCVK 180
DB 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAQCTDDYYRGHSAHIAIEKRSIQCVK 180
QY 181 LIVENGANVHARACGFFQKQGTCTFYFGLPLSLAACCTKQWDVVSYLENPHQPASLOA 240
DB 181 LIVENGANVHARACGFFQKQGTCTFYFGLPLSLAACCTKQWDVVSYLENPHQPASLOA 240
QY 241 TDSQGNVTLHALVMSIDNSAENIALVTSWYDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300
DB 241 TDSQGNVTLHALVMSIDNSAENIALVTSWYDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300

TDSQGNVTLHALVMSIDNSAENIALVTSWYDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300
AAKEGKIEIFRHILQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVEIITAF 360
AAKEGKIEIFRHILQREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVEIITAF 360
HCKSPHRHVMVLEPLNKLQAKWDLIIKPFNLCNLIYMFIFTAVAYHPTLKKQAA 420
HCKSPHRHVMVLEPLNKLQAKWDLIIKPFNLCNLIYMFIFTAVAYHPTLKKQAA 420
PHLKAEGVNSMLLTGHILGGLIYLLVQOLWYFWRHVFVIWISFIDSFEILFLFOALL 480
PHLKAEGVNSMLLTGHILGGLIYLLVQOLWYFWRHVFVIWISFIDSFEILFLFOALL 480
TVVSQVLCFLAEIWLPLVLSALVGLNLLYYTTRGFQHTGTYSMIQKVIIRDILLRFL 540
TVVSQVLCFLAEIWLPLVLSALVGLNLLYYTTRGFQHTGTYSMIQKVIIRDILLRFL 540
IYLVFLFGFAVALVLSQSEAWRPEAPTGPNTATESVQPMQEGDEGNGAQYRGILEASLEL 600
IYLVFLFGFAVALVLSQSEAWRPEAPTGPNTATESVQPMQEGDEGNGAQYRGILEASLEL 600
PKFTTGMGELAFQEQHFRGMVLLLLAYLLTYILLNMLIALMSETVNSVATDSWSIW 660
PKFTTGMGELAFQEQHFRGMVLLLLAYLLTYILLNMLIALMSETVNSVATDSWSIW 660
KLOKAI SVLEMBNGYWCRCRKQORAGVMTVGTGKPGSDERWCPRVEEVNWSWQTLPT 720
KLOKAI SVLEMBNGYWCRCRKQORAGVMTVGTGKPGSDERWCPRVEEVNWSWQTLPT 720
LCEDPSGAGVPRTLNPNVLASPPKDEDEGASEENVVPVQLQSN 764
LCEDPSGAGVPRTLNPNVLASPPKDEDEGASEENVVPVQLQSN 764

US-10-473-127-761
; Sequence 761, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 761
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-761

Query Match 100.0%; Score 4004; DB 16; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSSPVFRLETLDDGGQEDGSEADRGKLDGSGGLPPMESQFGEDRKFAPQIRVNLNY 60
DB 1 MTSPPSSPVFRLETLDDGGQEDGSEADRGKLDGSGGLPPMESQFGEDRKFAPQIRVNLNY 60
```

```
QY 61 RKGTSQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
DB 61 RKGTSQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
QY 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYGRGSHALHIAIEKRSIQCVK 180
DB 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYGRGSHALHIAIEKRSIQCVK 180
QY 181 LLVENGANVHARACGRFFQKGQGTCTFYFGEPLPLSLAACTKQMDVVSYLLENPHOPASLOA 240
DB 181 LLVENGANVHARACGRFFQKGQGTCTFYFGEPLPLSLAACTKQMDVVSYLLENPHOPASLOA 240
QY 241 TDSQGNVTVLHALVMI SDNSAENIALVTSMYDGLLOAGARLCPTVQLIEDIRNLDLTPLKL 300
DB 241 TDSQGNVTVLHALVMI SDNSAENIALVTSMYDGLLOAGARLCPTVQLIEDIRNLDLTPLKL 300
QY 301 AAKEGKIEIFRHILOREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
DB 301 AAKEGKIEIFRHILOREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
QY 361 HCKSPHRHRMVLEPLNKLLOAKWDLII PKFFLNFLCNLYMFIPTAVAYHOPTLKKQAA 420
DB 361 HCKSPHRHRMVLEPLNKLLOAKWDLII PKFFLNFLCNLYMFIPTAVAYHOPTLKKQAA 420
QY 421 PHLKAEVGNMMLTGHIILGGLYLLVQWQWYFMRHRHVFIIWISFIDSYPEILFLFOALL 480
DB 421 PHLKAEVGNMMLTGHIILGGLYLLVQWQWYFMRHRHVFIIWISFIDSYPEILFLFOALL 480
QY 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVIIRDLLRFL 540
DB 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVIIRDLLRFL 540
QY 541 IYLVFLGFAVALVSLSQEAWRPEATPGPNATESVQPMQEGDEGNGAQYRGILEASLEL 600
DB 541 IYLVFLGFAVALVSLSQEAWRPEATPGPNATESVQPMQEGDEGNGAQYRGILEASLEL 600
QY 601 FKFTIGMELAFQOLHFRGMVLLLLAYVLLTYVILLNMLIALMSETVNSVATDSWSIW 660
DB 601 FKFTIGMELAFQOLHFRGMVLLLLAYVLLTYVILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAI SVLEMENGYWMCCKKQAGVMLTVGTGPDGSPDRWCPRVEEVNWSWEQTLPT 720
DB 661 KLOKAI SVLEMENGYWMCCKKQAGVMLTVGTGPDGSPDRWCPRVEEVNWSWEQTLPT 720
QY 721 LCEDPGAGVPRTLENPVLASPPKDEDDGASEENYVPVQLQSN 764
DB 721 LCEDPGAGVPRTLENPVLASPPKDEDDGASEENYVPVQLQSN 764
```

RESULT 7

```
US-10-473-127-762
; Sequence 762, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE OF INVENTION: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 762
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-762

Query Match 100.0%; Score 4004; DB 16; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPSSSSVPRLETLDDGGQDGEADRGKLDGSGLPMMESQFQGEDRKFAFQIRVNLNY 60
DB 1 MTPSSSSVPRLETLDDGGQDGEADRGKLDGSGLPMMESQFQGEDRKFAFQIRVNLNY 60
QY 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
DB 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
QY 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYGRGSHALHIAIEKRSIQCVK 180
DB 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYGRGSHALHIAIEKRSIQCVK 180
QY 181 LLVENGANVHARACGRFFQKGQGTCTFYFGEPLPLSLAACTKQMDVVSYLLENPHOPASLOA 240
DB 181 LLVENGANVHARACGRFFQKGQGTCTFYFGEPLPLSLAACTKQMDVVSYLLENPHOPASLOA 240
QY 241 TDSQGNVTVLHALVMI SDNSAENIALVTSMYDGLLOAGARLCPTVQLIEDIRNLDLTPLKL 300
DB 241 TDSQGNVTVLHALVMI SDNSAENIALVTSMYDGLLOAGARLCPTVQLIEDIRNLDLTPLKL 300
QY 301 AAKEGKIEIFRHILOREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
DB 301 AAKEGKIEIFRHILOREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIF 360
QY 361 HCKSPHRHRMVLEPLNKLLOAKWDLII PKFFLNFLCNLYMFIPTAVAYHOPTLKKQAA 420
DB 361 HCKSPHRHRMVLEPLNKLLOAKWDLII PKFFLNFLCNLYMFIPTAVAYHOPTLKKQAA 420
QY 421 PHLKAEVGNMMLTGHIILGGLYLLVQWQWYFMRHRHVFIIWISFIDSYPEILFLFOALL 480
DB 421 PHLKAEVGNMMLTGHIILGGLYLLVQWQWYFMRHRHVFIIWISFIDSYPEILFLFOALL 480
QY 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVIIRDLLRFL 540
DB 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVIIRDLLRFL 540
QY 541 IYLVFLGFAVALVSLSQEAWRPEATPGPNATESVQPMQEGDEGNGAQYRGILEASLEL 600
DB 541 IYLVFLGFAVALVSLSQEAWRPEATPGPNATESVQPMQEGDEGNGAQYRGILEASLEL 600
QY 601 FKFTIGMELAFQOLHFRGMVLLLLAYVLLTYVILLNMLIALMSETVNSVATDSWSIW 660
DB 601 FKFTIGMELAFQOLHFRGMVLLLLAYVLLTYVILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAI SVLEMENGYWMCCKKQAGVMLTVGTGPDGSPDRWCPRVEEVNWSWEQTLPT 720
DB 661 KLOKAI SVLEMENGYWMCCKKQAGVMLTVGTGPDGSPDRWCPRVEEVNWSWEQTLPT 720
QY 721 LCEDPGAGVPRTLENPVLASPPKDEDDGASEENYVPVQLQSN 764
DB 721 LCEDPGAGVPRTLENPVLASPPKDEDDGASEENYVPVQLQSN 764
```

RESULT 8

```
US-10-473-127-765
; Sequence 765, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE OF INVENTION: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
```



```
QY 541 IYLVFLGFAVALVSLQSARWPEAFTGNATESVQPMGQDEGNGAQRGILEASLEL 600
DB 541 IYLVFLGFAVALVSLQSARWPEAFTGNATESVQPMGQDEGNGAQRGILEASLEL 600
QY 601 FKFTTGMGELAFQEQQLHFRGMVLLLLAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660
DB 601 FKFTTGMGELAFQEQQLHFRGMVLLLLAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAI SVLEMENGYWCRKQKQAGVMLTVGTPDGS PDERWCFRVEEVNWNASWEQTLP 720
DB 661 KLOKAI SVLEMENGYWCRKQKQAGVMLTVGTPDGS PDERWCFRVEEVNWNASWEQTLP 720
QY 721 LCEDPSGAGVPRTLENPVLASPPKEDGSEBENYVPVQLQSN 764
DB 721 LCEDPSGAGVPRTLENPVLASPPKEDGSEBENYVPVQLQSN 764

RESULT 10
US-10-473-127-772
; Sequence 772, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 772
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-772

Query Match 100.0%; Score 4004; DB 16; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPSSSPVFRLETLDDGGQDSEADRGKLD FSGSLPPMESQFGEDRKFPQIRVNLNY 60
DB 1 MTSPSSSPVFRLETLDDGGQDSEADRGKLD FSGSLPPMESQFGEDRKFPQIRVNLNY 60
QY 61 RKG TGASQPDNRRDRRLFNVRGVPEDLAGLPEYLSKTSKYLTDSYETEGSTGKTCL 120
DB 61 RKG TGASQPDNRRDRRLFNVRGVPEDLAGLPEYLSKTSKYLTDSYETEGSTGKTCL 120
QY 121 MKAVLNKDGYNACILPLQIDRDSGNPQPLVNAQCTDDYRHSALHIAIEKRSLOCVK 180
DB 121 MKAVLNKDGYNACILPLQIDRDSGNPQPLVNAQCTDDYRHSALHIAIEKRSLOCVK 180
QY 181 LLVENGANVHARACGRFFKQGGTCFYFGEPLSLAACKQDWVSVYLLNPHQPASLOA 240
DB 181 LLVENGANVHARACGRFFKQGGTCFYFGEPLSLAACKQDWVSVYLLNPHQPASLOA 240
QY 241 TDSQGNVTHALVMSDMSANIALVTSWYDGLLQAGARLCTPTVOLEDIRNLQDLTPKL 300
DB 241 TDSQGNVTHALVMSDMSANIALVTSWYDGLLQAGARLCTPTVOLEDIRNLQDLTPKL 300
QY 301 AAKEGKIEIFRHILOREFSGLSHRKFTWCYGPVRVSLYDLASVDSCEENSYLEIIAF 360
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DB 301 AAKEGKIEIFRHILOREFSGLSHRKFTWCYGPVRVSLYDLASVDSCEENSYLEIIAF 360
QY 361 HCKSPHRHRMVVLEPLNKLQAKWDLIPKPFNLFCNLIYNFI FTAVAYHOPTLKQOAA 420
DB 361 HCKSPHRHRMVVLEPLNKLQAKWDLIPKPFNLFCNLIYNFI FTAVAYHOPTLKQOAA 420
QY 421 PHLKA EVGNSMLLTGHILILGGIYLLVGQLWYFWRHRVFIWISFIDSYFEILFLFOALL 480
DB 421 PHLKA EVGNSMLLTGHILILGGIYLLVGQLWYFWRHRVFIWISFIDSYFEILFLFOALL 480
QY 481 TVVSQVLCFLAEWVLP LLVSALVGLWNLIIYTRGFQHTGIYSVMIOKVILRDLRLLELL 540
DB 481 TVVSQVLCFLAEWVLP LLVSALVGLWNLIIYTRGFQHTGIYSVMIOKVILRDLRLLELL 540
QY 541 IYLVFLGFAVALVSLQSARWPEAFTGNATESVQPMGQDEGNGAQRGILEASLEL 600
DB 541 IYLVFLGFAVALVSLQSARWPEAFTGNATESVQPMGQDEGNGAQRGILEASLEL 600
QY 601 FKFTTGMGELAFQEQQLHFRGMVLLLLAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660
DB 601 FKFTTGMGELAFQEQQLHFRGMVLLLLAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAI SVLEMENGYWCRKQKQAGVMLTVGTPDGS PDERWCFRVEEVNWNASWEQTLP 720
DB 661 KLOKAI SVLEMENGYWCRKQKQAGVMLTVGTPDGS PDERWCFRVEEVNWNASWEQTLP 720
QY 721 LCEDPSGAGVPRTLENPVLASPPKEDGSEBENYVPVQLQSN 764
DB 721 LCEDPSGAGVPRTLENPVLASPPKEDGSEBENYVPVQLQSN 764

RESULT 11
US-10-473-127-776
; Sequence 776, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 776
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-776

Query Match 100.0%; Score 4004; DB 16; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPSSSPVFRLETLDDGGQDSEADRGKLD FSGSLPPMESQFGEDRKFPQIRVNLNY 60
DB 1 MTSPSSSPVFRLETLDDGGQDSEADRGKLD FSGSLPPMESQFGEDRKFPQIRVNLNY 60
QY 61 RKG TGASQPDNRRDRRLFNVRGVPEDLAGLPEYLSKTSKYLTDSYETEGSTGKTCL 120
DB 61 RKG TGASQPDNRRDRRLFNVRGVPEDLAGLPEYLSKTSKYLTDSYETEGSTGKTCL 120
```

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QY 121 MKAVNLKDGVNACILPLQIDRDSGNPQPLVNAOCTDDYRHSALHIAIEKRSIQCVK 180
Db 121 MKAVNLKDGVNACILPLQIDRDSGNPQPLVNAOCTDDYRHSALHIAIEKRSIQCVK 180
QY 181 LLVENGANVHARACGRFFQKGQGTCTFYFGLPLSLAACTKQWDVSVYLLNPHOPASLOA 240
Db 181 LLVENGANVHARACGRFFQKGQGTCTFYFGLPLSLAACTKQWDVSVYLLNPHOPASLOA 240
QY 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCTVQLEDIRNLQDLTFLKL 300
Db 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCTVQLEDIRNLQDLTFLKL 300
QY 301 AAKEGKIEIPRHILQREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIAF 360
Db 301 AAKEGKIEIPRHILQREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIAF 360
QY 361 HCKSPHRRHVMVLEPLNKLQAKWDLILPKFFLNFCLNLIYMFIFTAVAYHQP TLKQAA 420
Db 361 HCKSPHRRHVMVLEPLNKLQAKWDLILPKFFLNFCLNLIYMFIFTAVAYHQP TLKQAA 420
QY 421 PHLKAEGVNSMLTGHILILGGIYLLVGLQWYFRRHVFIWISFIDSYPFEILFLFOALL 480
Db 421 PHLKAEGVNSMLTGHILILGGIYLLVGLQWYFRRHVFIWISFIDSYPFEILFLFOALL 480
QY 481 TVVSQVLCFLAIEMWYLPPLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVILRDLLRFL 540
Db 481 TVVSQVLCFLAIEMWYLPPLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVILRDLLRFL 540
QY 541 IYLVFLGFAVALVSLSOEAWRPEAPTGNATESVQPMEGQDEGNGAQYRGILEASLEL 600
Db 541 IYLVFLGFAVALVSLSOEAWRPEAPTGNATESVQPMEGQDEGNGAQYRGILEASLEL 600
QY 601 FKFTIGMGEALFAOEQLHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
Db 601 FKFTIGMGEALFAOEQLHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLQKAI SVLEMENGYWCRKKQKQAGVMLTVGTPDGS PDERWCFRVEEVNWSWEGTLPT 720
Db 661 KLQKAI SVLEMENGYWCRKKQKQAGVMLTVGTPDGS PDERWCFRVEEVNWSWEGTLPT 720
QY 721 LCEDPSGAGVPRTLENPVLASPPKEDDGEASENYPVQLQSN 764
Db 721 LCEDPSGAGVPRTLENPVLASPPKEDDGEASENYPVQLQSN 764

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RESULT 12

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US-10-473-127-779
; Sequence 779, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 779
; LENGTH: 764
; TYPE: PRT

```

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; ORGANISM: Homo sapiens
US-10-473-127-779

```

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Query Match 100.0%; Score 4004; DB 16; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MTSPPSSPVFRLETLDGQEDGSEADRGKLDGSGLPMPMESQFQGEDRKPFAQIRVNLNY 60
Db 1 MTSPPSSPVFRLETLDGQEDGSEADRGKLDGSGLPMPMESQFQGEDRKPFAQIRVNLNY 60
QY 61 RGTGASQSDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSTYTGSGTKTCL 120
Db 61 RGTGASQSDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSTYTGSGTKTCL 120
QY 121 MKAVNLKDGVNACILPLQIDRDSGNPQPLVNAOCTDDYRHSALHIAIEKRSIQCVK 180
Db 121 MKAVNLKDGVNACILPLQIDRDSGNPQPLVNAOCTDDYRHSALHIAIEKRSIQCVK 180
QY 181 LLVENGANVHARACGRFFQKGQGTCTFYFGLPLSLAACTKQWDVSVYLLNPHOPASLOA 240
Db 181 LLVENGANVHARACGRFFQKGQGTCTFYFGLPLSLAACTKQWDVSVYLLNPHOPASLOA 240
QY 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCTVQLEDIRNLQDLTFLKL 300
Db 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCTVQLEDIRNLQDLTFLKL 300
QY 301 AAKEGKIEIPRHILQREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIAF 360
Db 301 AAKEGKIEIPRHILQREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEENSVLBIIAF 360
QY 361 HCKSPHRRHVMVLEPLNKLQAKWDLILPKFFLNFCLNLIYMFIFTAVAYHQP TLKQAA 420
Db 361 HCKSPHRRHVMVLEPLNKLQAKWDLILPKFFLNFCLNLIYMFIFTAVAYHQP TLKQAA 420
QY 421 PHLKAEGVNSMLTGHILILGGIYLLVGLQWYFRRHVFIWISFIDSYPFEILFLFOALL 480
Db 421 PHLKAEGVNSMLTGHILILGGIYLLVGLQWYFRRHVFIWISFIDSYPFEILFLFOALL 480
QY 481 TVVSQVLCFLAIEMWYLPPLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVILRDLLRFL 540
Db 481 TVVSQVLCFLAIEMWYLPPLVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVILRDLLRFL 540
QY 541 IYLVFLGFAVALVSLSOEAWRPEAPTGNATESVQPMEGQDEGNGAQYRGILEASLEL 600
Db 541 IYLVFLGFAVALVSLSOEAWRPEAPTGNATESVQPMEGQDEGNGAQYRGILEASLEL 600
QY 601 FKFTIGMGEALFAOEQLHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
Db 601 FKFTIGMGEALFAOEQLHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLQKAI SVLEMENGYWCRKKQKQAGVMLTVGTPDGS PDERWCFRVEEVNWSWEGTLPT 720
Db 661 KLQKAI SVLEMENGYWCRKKQKQAGVMLTVGTPDGS PDERWCFRVEEVNWSWEGTLPT 720
QY 721 LCEDPSGAGVPRTLENPVLASPPKEDDGEASENYPVQLQSN 764
Db 721 LCEDPSGAGVPRTLENPVLASPPKEDDGEASENYPVQLQSN 764

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RESULT 13

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US-10-915-017-36
; Sequence 36, Application US/10915017
; Publication No. US20050095650A1
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: UCSF-084CON2
; CURRENT APPLICATION NUMBER: US/10/915,017

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; CURRENT FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: 09/978,303
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-915-017-36

Query Match      100.0%; Score 4004; DB 17; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSPVFRLETLDDGGQDGEADRGKLDGSGGLPPMESQFGQDRKFAPOIRVNLNY 60
DB 1 MTSPPSPVFRLETLDDGGQDGEADRGKLDGSGGLPPMESQFGQDRKFAPOIRVNLNY 60
QY 61 RKG TGASQDPNRFDRDLFNAVSRGVDPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
DB 61 RKG TGASQDPNRFDRDLFNAVSRGVDPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
QY 121 MKAVLNKDGVNACILPLQIDRDSGNPQPLVNAQCTDDYRGRSHALHIAIEKRSLQCVK 180
DB 121 MKAVLNKDGVNACILPLQIDRDSGNPQPLVNAQCTDDYRGRSHALHIAIEKRSLQCVK 180
QY 181 LLVENGANVHARACGRFFQKGQGTCTFYFGLPELSLAAC TKQMDVSYLLENPHOPASLOA 240
DB 181 LLVENGANVHARACGRFFQKGQGTCTFYFGLPELSLAAC TKQMDVSYLLENPHOPASLOA 240
QY 241 TDSQGN TVLHALVMSIDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300
DB 241 TDSQGN TVLHALVMSIDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300
QY 301 AAKEGKIEIFRHILOREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEANSVLEIIAF 360
DB 301 AAKEGKIEIFRHILOREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEANSVLEIIAF 360
QY 361 HCKSPHRHVMVLEPLNKLLQAKWDLIIPKFFLNFLCNLYMFI FTAVAVHQTPLKKQAA 420
DB 361 HCKSPHRHVMVLEPLNKLLQAKWDLIIPKFFLNFLCNLYMFI FTAVAVHQTPLKKQAA 420
QY 421 PHLKAEGVNSMLLTGHILILGGIYLLVGQLYFWRRHVFIIWISFIDSYPEILFLFQALL 480
DB 421 PHLKAEGVNSMLLTGHILILGGIYLLVGQLYFWRRHVFIIWISFIDSYPEILFLFQALL 480
QY 481 TVVSQVLCFLAIEWYLP LLSALVGLWNL LLYYTRGFQHTGTGIYSVMIQKVL RDLLRFL 540
DB 481 TVVSQVLCFLAIEWYLP LLSALVGLWNL LLYYTRGFQHTGTGIYSVMIQKVL RDLLRFL 540
QY 541 IYLVFLGFAVALVSLSQEAWRPEAPTGNATESVQMEQDEGNGA YRGILEASLEL 600
DB 541 IYLVFLGFAVALVSLSQEAWRPEAPTGNATESVQMEQDEGNGA YRGILEASLEL 600
QY 601 FKFTIGMELAFQQLFRGVM LLLAYVLLTVLLNLMLIALMSVTNSVATDSWSIW 660
DB 601 FKFTIGMELAFQQLFRGVM LLLAYVLLTVLLNLMLIALMSVTNSVATDSWSIW 660
QY 661 KLOKAI SVLEMENGYWCRKKQKQAGVMLTVGT KPDGSPDRWC FRVEEVNVA SWEQTLPT 720
DB 661 KLOKAI SVLEMENGYWCRKKQKQAGVMLTVGT KPDGSPDRWC FRVEEVNVA SWEQTLPT 720
QY 721 LCEDPGAGVPR TLENVILASPPKDEDEGAS EENYVPVQLQSN 764
DB 721 LCEDPGAGVPR TLENVILASPPKDEDEGAS EENYVPVQLQSN 764

US-11-013-090-5
; Sequence 5, Application US/11013090
; Publication No. US20050158827A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICATOR: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
; FILE REFERENCE: MPI98-093P2RCP3DV1AM
; CURRENT APPLICATION NUMBER: US/11/013,090
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: US 09/439,165
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/421,134
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 09/258,633
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: US 60/114,078
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/108,322
; PRIOR FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-013-090-5

Query Match      100.0%; Score 4004; DB 20; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSPVFRLETLDDGGQDGEADRGKLDGSGGLPPMESQFGQDRKFAPOIRVNLNY 60
DB 1 MTSPPSPVFRLETLDDGGQDGEADRGKLDGSGGLPPMESQFGQDRKFAPOIRVNLNY 60
QY 61 RKG TGASQDPNRFDRDLFNAVSRGVDPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
DB 61 RKG TGASQDPNRFDRDLFNAVSRGVDPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
QY 121 MKAVLNKDGVNACILPLQIDRDSGNPQPLVNAQCTDDYRGRSHALHIAIEKRSLQCVK 180
DB 121 MKAVLNKDGVNACILPLQIDRDSGNPQPLVNAQCTDDYRGRSHALHIAIEKRSLQCVK 180
QY 181 LLVENGANVHARACGRFFQKGQGTCTFYFGLPELSLAAC TKQMDVSYLLENPHOPASLOA 240
DB 181 LLVENGANVHARACGRFFQKGQGTCTFYFGLPELSLAAC TKQMDVSYLLENPHOPASLOA 240
QY 241 TDSQGN TVLHALVMSIDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300
DB 241 TDSQGN TVLHALVMSIDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300
QY 301 AAKEGKIEIFRHILOREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEANSVLEIIAF 360
DB 301 AAKEGKIEIFRHILOREFSGLSHLRKFTWCYGPVRVSLYDLASVDSCEANSVLEIIAF 360
QY 361 HCKSPHRHVMVLEPLNKLLQAKWDLIIPKFFLNFLCNLYMFI FTAVAVHQTPLKKQAA 420
DB 361 HCKSPHRHVMVLEPLNKLLQAKWDLIIPKFFLNFLCNLYMFI FTAVAVHQTPLKKQAA 420
QY 421 PHLKAEGVNSMLLTGHILILGGIYLLVGQLYFWRRHVFIIWISFIDSYPEILFLFQALL 480
DB 421 PHLKAEGVNSMLLTGHILILGGIYLLVGQLYFWRRHVFIIWISFIDSYPEILFLFQALL 480
QY 481 TVVSQVLCFLAIEWYLP LLSALVGLWNL LLYYTRGFQHTGTGIYSVMIQKVL RDLLRFL 540
DB 481 TVVSQVLCFLAIEWYLP LLSALVGLWNL LLYYTRGFQHTGTGIYSVMIQKVL RDLLRFL 540
QY 541 IYLVFLGFAVALVSLSQEAWRPEAPTGNATESVQMEQDEGNGA YRGILEASLEL 600
DB 541 IYLVFLGFAVALVSLSQEAWRPEAPTGNATESVQMEQDEGNGA YRGILEASLEL 600
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Qy 601 FKFTTGMGELAFQEQHFRGMVLLLLAVVLLTYILLNNMLIALMSETVNSVATDSWSIW 660
Db 601 FKFTTGMGELAFQEQHFRGMVLLLLAVVLLTYILLNNMLIALMSETVNSVATDSWSIW 660

Qy 661 KLOKALISVLEMENGYWCKKQKQAGVMLTVGTPDGSPPDERMCFRVEEVNMAWSEOTLPT 720
Db 661 KLOKALISVLEMENGYWCKKQKQAGVMLTVGTPDGSPPDERMCFRVEEVNMAWSEOTLPT 720

Qy 721 LCEDPGAGVPRTLNPNVLASPPKEDGEGASEENYVPVQLQSN 764
Db 721 LCEDPGAGVPRTLNPNVLASPPKEDGEGASEENYVPVQLQSN 764

RESULT 15
US-10-168-651-3
; Sequence 3, Application US/10168651
; Publication No. US20030171275A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyoung Aina M.
; APPLICANT: YANG, Junming
; APPLICANT: REDDY, Roopa
; APPLICANT: LAL, Preeti
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: YUE, Henry
; APPLICANT: NGUYEN, Dannie B.
; APPLICANT: YAO, Monique G.
; APPLICANT: GANDHI, Ameen R.
; APPLICANT: TANG, Y. Tom
; APPLICANT: KHAN, Farrah A.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0005 PCT
; CURRENT APPLICATION NUMBER: US/10/168,651
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/172,000; 60/176,083; 60/177,332; 60/178,572; 60/179,758;
; 60/181,625
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-21; 2000-01-28; 2000-02-02;
; 2000-02-10
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030171275A1 2446438CD1
US-10-168-651-3

Query Match 99.9%; Score 3998; DB 14; Length 764;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 763; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTSFSSPVFRLETLDGQGDGSEADRGKLDGSGLPMPMESQFGEDRKFPQIRVNLNY 60
Db 1 MTSFSSPVFRLETLDGQGDGSEADRGKLDGSGLPMPMESQFGEDRKFPQIRVNLNY 60

Qy 61 RKGTGASQDPNFRDRRLFNVAHSVGPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
Db 61 RKGTGASQDPNFRDRRLFNVAHSVGPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120

Qy 121 MKAVLNKQGVNACILPLQIDRDSGNPQPLVNAQCTDDYRGHSALHIAIEKRSLOQVK 180
Db 121 MKAVLNKQGVNACILPLQIDRDSGNPQPLVNAQCTDDYRGHSALHIAIEKRSLOQVK 180

Qy 181 LLVENGANVHARACGRFFQKQGCTCFYFGELPLSLAACTQKQWDVSVYLLLENPHQPASLOA 240
Db 181 LLVENGANVHARACGRFFQKQGCTCFYFGELPLSLAACTQKQWDVSVYLLLENPHQPASLOA 240

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Qy 241 TDSQNTVVLHALVMI SDNSAENIALVTSMYDGLLOAGARLCTPVOLEDIRNLODITPLKL 300
Db 241 TDSQNTVVLHALVMI SDNSAENIALVTSMYDGLLOAGARLCTPVOLEDIRNLODITPLKL 300

Qy 301 AAKEGKIIFRHILOREFSGLSHLRKTEWCYGPVRVSLYDLASVDSCEENSVELEIAF 360
Db 301 AAKEGKIIFRHILOREFSGLSHLRKTEWCYGPVRVSLYDLASVDSCEENSVELEIAF 360

Qy 361 HCKSPHRHRMVVLEPLANKLLOAKWDLIPKPFNLFLCNLIYMFIFTAVAYHPTLKKQAA 420
Db 361 HCKSPHRHRMVVLEPLANKLLOAKWDLIPKPFNLFLCNLIYMFIFTAVAYHPTLKKQAA 420

Qy 421 PHLKAEGNSMLLTGHILILGGIYLLVQOLWYFRRHVFIWISFIDSFEILFQALL 480
Db 421 PHLKAEGNSMLLTGHILILGGIYLLVQOLWYFRRHVFIWISFIDSFEILFQALL 480

Qy 481 TVVSQVLCFLAJEMWYLLPLLSALVLGWLNLNLYYTRGFQHTGIYSVMIQKVILRDLRLFLL 540
Db 481 TVVSQVLCFLAJEMWYLLPLLSALVLGWLNLNLYYTRGFQHTGIYSVMIQKVILRDLRLFLL 540

Qy 541 IYLVFLPGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGQDEGNGAQYRGILEASLEL 600
Db 541 IYLVFLPGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGQDEGNGAQYRGILEASLEL 600

Qy 601 FKFTTGMGELAFQEQHFRGMVLLLLAVVLLTYILLNNMLIALMSETVNSVATDSWSIW 660
Db 601 FKFTTGMGELAFQEQHFRGMVLLLLAVVLLTYILLNNMLIALMSETVNSVATDSWSIW 660

Qy 661 KLOKALISVLEMENGYWCKKQKQAGVMLTVGTPDGSPPDERMCFRVEEVNMAWSEOTLPT 720
Db 661 KLOKALISVLEMENGYWCKKQKQAGVMLTVGTPDGSPPDERMCFRVEEVNMAWSEOTLPT 720

Qy 721 LCEDPGAGVPRTLNPNVLASPPKEDGEGASEENYVPVQLQSN 764
Db 721 LCEDPGAGVPRTLNPNVLASPPKEDGEGASEENYVPVQLQSN 764

```

Search completed: October 5, 2005, 11:37:13
Job time : 171 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2005, 11:13:10 ; Search time 20 Seconds
(without alignments)
3675.480 Million cell updates/sec

Title: US-09-445-614B-2
Perfect score: 4004
Sequence: 1 MTPSSSPVRLTLGGQE.....EDEDGASENYPVQLQSN 764

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1652	41.3	838	2 T09054	capsaicin receptor
2	1651.5	41.2	839	2 JC7621	capsaicin receptor
3	634	15.8	725	2 JC7531	calcium transport
4	615.5	15.4	727	2 JC7796	epithelial calcium
5	581	14.5	723	2 JC7795	epithelial calcium
6	414	10.3	900	2 T33026	hypothetical prote
7	382.5	9.8	790	2 T20312	hypothetical prote
8	365.5	9.1	957	2 D88651	protein B0212.5 [i
9	364	9.1	937	2 T37241	olfactory channel
10	261	6.5	519	2 T24772	hypothetical prote
11	209	5.2	1188	2 T19552	hypothetical prote
12	197.5	4.9	1124	2 JH0588	calmodulin-binding
13	191	4.8	1274	2 JN0015	trp protein - fru
14	190.5	4.8	1275	2 JU0092	trp protein - fru
15	174	4.3	810	2 T38361	TRPC1 protein - hu
16	167.5	4.2	934	1 H71274	hypothetical prote
17	157.5	3.9	481	2 T23729	hypothetical prote
18	157	3.9	1549	2 T13940	ankyrin - fruit fl
19	151	3.8	1765	2 T42714	ankyrin 3, splice
20	151	3.8	1940	2 T42715	ankyrin 3, splice
21	151	3.8	1943	2 T42713	ankyrin 3, splice
22	151	3.8	1961	2 T42716	ankyrin 3, splice
23	151	3.8	3924	2 T37431	ankyrin 2, neuroa
24	150.5	3.8	793	2 S86238	trp-1 protein - hu
25	150	3.7	887	2 T03939	potassium channel
26	150	3.7	4377	2 A55575	ankyrin 3, long sp
27	147	3.7	1001	2 S30385	G9a protein - huma
28	145.5	3.6	899	2 F88391	protein R0610.4 [
29	144.5	3.6	2004	2 D88948	protein ZK1005.1 [

RESULT 1
T09054
capsaicin receptor - rat
N;Alternate names: vanilloid receptor subtype 1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09054
R;Caterina, M.J.; Schumacher, M.A.; Tominaga, M.; Rosen, T.A.; Levine, J.D.; Julius, D.
Nature 389, 816-824, 1997
A;Title: The capsaicin receptor: A heat-activated ion channel in the pain pathway.
A;Reference number: Z16539; MUID:98007969; PMID:9349813
A;Accession: T09054
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-838 <CAT>
A;Cross-references: UNIPROT:Q35433; EMBL:AF029310; NID:G2570932; PIDN:AAC53398.1; PID:G
A;Experimental source: dorsal root ganglion
C;Keywords: ion channel; receptor

Query Match 41.3%; Score 1652; DB 2; Length 838;
Best Local Similarity 46.3%; Pred.No. 5.5e-120;
Matches 359; Conservative 127; Mismatches 230; Indels 60; Gaps 15;

Qy	18	GOBDSGSEADRGKLDGFGSLPPMESQFOGEDRKFAPIQIRVN---	LNRYKRGTG-----	65
Db	51	GKGDSEAS-----	PLDCPYEEGLASCPITVSSVLTIQRPDGPASVRPSSQ	99
Qy	66	-----ASQPDNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSYETSGSTGKTCLM	121	
Db	100	DSVSAGEKPPRLYDRRSIFDAVAQSNCOELESLLPFLQRSKRLTDSFKDPETGKTCLL	159	
Qy	122	KAVLNKDGYNACILPLQIDRDGNGPQPLVNAOCTDDYRGHSALHIAIEKRSLOCVKL	181	
Db	160	KAMLNHNGQNDTIALLLDVARKTDSLQKFNASYSYKGGQTALHIAIERRNWLTVL	219	
Qy	182	LVENGANVHARACGRPFQKQGG--TCFYFGLPLSLAACTQMDVWVSVYLLNPHOPASLOA	240	
Db	220	LVENGADVOQAANGDFFKTKGRPGFYFGLPLSLAACTQALVAVKFLQNSWQPADISA	279	
Qy	241	TDSQGNVTLHALVMSIDNSAENIALVTSMYDGLLOAGARLCPVTOLEDIRNLQDLTPLKL	300	
Db	280	RDSVGNVTLHALVEVADNTVDNTKFVTSMYNEILLGAKLHPTLKLBEITNRKGLTPLAL	339	
Qy	301	AAKEGKTEIFRHILQREF--SGLSHLSRKFTWCYGVPRVSLYDLASVDSCEENSVLBI	358	
Db	340	AASGKIGVLAYILQREIHEPECHLSRKFTWYAGPVHSSLYDLSCIDTCEKNSVLEVI	399	
Qy	359	AF-HCKSPHRRMVVLEPLNKLQAKWDLIPK--FFLNFLCNLIYMFIFTAVAYHQPTLK	416	
Db	400	AYSSSTPNRHDMLLVEPLNLLQDKWDRFVKRIFYFNFFVYCLYMIIFTAAAYRPPV--	457	
Qy	417	KQAAP--HLKAEVGNMMLTGHILLGGIYLLVQLWYFWRHNVFWMISIDTSFYELF	474	

ALIGNMENTS


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Db 458 -EGLPPYKKNVTGDFRVVTEGILSVGGVYFFRRGIQFLQRRPDKSLFVDSYSEILP 516
QY 475 LFOALLTVVSQVLCFLAIEAWYLLVLSALVGLWNLNLYYTRGFQHTGTGIYSVMIQVILRD 534
Db 517 FVQSLFWLVSVLVYFSQRKEYVASVFLSANGTWNMLYYTRGFQNGGIYAVMIEKMLRD 576
QY 535 LURFLIYLVFLPGFAVALVLSQEAWRPEAPFGPNATESVQPMGEQDEGNA-----588
Db 577 LCRFMFVLVFLPGFSTAVVTLIED-----GKN---NSLPMESTPHKCRGSACKPGN 625
QY 589 QYRGILEASLEPKFTIGWELAFQOLHFRGMVLLLLAYVLLTYILLNMLIALMSGT 648
Db 626 SYNSLSYTCLELFPKFTIGWDLFTENYDFKAVFIILLAYVLLTYILLNMLIALMGET 685
QY 649 VNSVATDSMSIWKLQKAISVLEMGYWC-RKKQAGVMLTVGTPDGSPPDERWCFRVE 707
Db 686 VNKIAQESKNWKLQRAITILDTKESFLKCMKAFRSGLLQVGFPPDGKDDYRWCFRVD 745
QY 708 EVNWASWEOTLPTLCEDPSGA-GVPRTLENVPLASPPKDEBDGASENVVPVOLLQ 762
Db 746 EVNWTTWNTVGIINBDPGNCEGVKRTLSFSLRS---RVSGRNKNFALVPLLR 797

RESULT 2
JC7621
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7621
R;Cortright, D.N.; Crandall, M.; Sanchez, J.F.; Zou, T.; Krause, J.E.; White, G.
Biochem. Biophys. Res. Commun. 281, 1183-1189, 2001
A;Title: The tissue distribution and functional characterization of human VR1.
A;Reference number: JC7621; MUID:21139751; PMID:11243859
A;Contents: Dorsal root ganglia
A;Accession: JC7621
A;Molecule type: mRNA
A;Residues: 1-839 <OR>
A;Cross-references: UNIPROT:Q9H304; GB:AF196175
C;Comment: This receptor, a transmembrane protein with many phosphorylation sites, is a
its integrative activation by several noxious stimuli, and plays an important role in ir
C;Genetics:
A;Gene: vr1
A;Map position: 17p13
C;Keywords: transmembrane protein
F;201-233/Domain: ankyrin #status predicted <ANK1>
F;248-280/Domain: ankyrin #status predicted <ANK2>
F;333-365/Domain: ankyrin #status predicted <ANK3>
F;433-455/Domain: transmembrane #status predicted <TM1>
F;477-495/Domain: transmembrane #status predicted <TM2>
F;508-531/Domain: transmembrane #status predicted <TM3>
F;543-569/Domain: transmembrane #status predicted <TM4>
F;578-597/Domain: transmembrane #status predicted <TM5>
F;624-644/Region: pore loop #status predicted
F;656-684/Domain: transmembrane #status predicted <TM6>

Query Match 41.2%; Score 1651.5; DB 2; Length 839;
Best Local Similarity 48.5%; Pred. No. 6.1e-120;
Matches 344; Conservative 122; Mismatches 199; Indels 45; Gaps 11;

QY 74 FDRRLFNVAVRGVPEDLAGLPYLSKTSKYLTDSEYTEGSTGKTCLMKAVLNKDGUNA 133
Db 113 YDRRSIFEVAQNQCQDLSELLLFLQKSKHLLDNEFPDTPETGKTLKAMLNLDHGQNT 172
QY 134 CILPLQLDRDGNPQPLVNAQCTDDYTRGHSALHTAIEKRSQCQVKLVVENGANYHARA 193
Db 173 TIPLLIEARQTSKLLENVNASYDTSYKQTAHTAIERNNVALVTLLVENGADVQAAA 232
QY 194 CGRFFQKQGC-TCFYFGELPLSLAACTKQWDVVSYLENPHQPASLQATDSQGNTVLHAL 252
Db 233 HGDFFPKTKRPGFYGELPLSLAACTNQLGIKVELLQNSWQTADISARDSVGNTVLHAL 292
QY 253 VMTSDNSAENIALVTSYMDGLLQAGRLCTVQLEDIRNLQDITPLKLAKEGKIEIFRH 312
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Db 293 VEVAQNTADNTKFTVSMNEILMLGAKLHPTLKLEELTNKKGMTPLAALAGTGKIGLAY 352
QY 313 ILQREFS--GLSHLSRKFTWCYGPVRVSLVDLASVDSCEENSVLEIIAF-HCKSPHRRH 369
Db 353 ILQREIQBPCECHLSRKFTWAYGVPVHSLYDLSDICDTCEKNSVLEIAYSSSETPNRHD 412
QY 370 MVVLEPLNKLQAKWDLIPK-FFLNFLCNLIYMEIFTAVAHQPTLKQAAAPHLKAE-V 427
Db 413 MLLVLEPLNRLQDKWDRFVKRIFYFNFLVYCLYMIIFTMAAYRVRV--DGLPPPFMEKI 469
QY 428 GNSMLLTGTHILILGIGVLLVGLQWYFWRRHVFIIWSFIDSYFEILFLFOALLTVVSQVL 487
Db 470 GYFRTVTEGILSVLGVYFFFGIOYFLQRRPSMKTFLVDSYSEMLFFLOSLFMLATVVL 529
QY 488 CFLAIEWLPLLVLSALVGLWNLNLYYTRGFQHTGTGIYSVMIQVILRDLLRFLIYLVL 547
Db 530 YFSLKEVVASVVSFSLALGWTNMLYYTRGFQMGIVAVMIEKMLRDLCRFMFVIVFLF 589
QY 548 GFAVALVLSQEA-----WRPEAPTGNATESVQPMGEQDEGNAQYRGIL 594
Db 590 GFSTAVVTLIEDGKNDSLPSSESTSHRWGPACRPPDSS-----YNSLY 632
QY 595 EASLELFKFTIGWELAFQOLHFRGMVLLLLAYVLLTYILLNMLIALMSSETVNSVAT 654
Db 633 STCLSELFKFTIGWDLFTENYDFKAVFIILLAYVLLTYILLNMLIALMGETVNKIAQ 692
QY 655 DSWSIWKLQKAISVLEMGYWC-RKKQAGVMLTVGTPDGSPPDERWCFRVEVNNAS 713
Db 693 ESKNIWKLQRAITILDTKESFLKCMKAFRSGLLQVGYTPDGKDDYRWCFRVDEVNWT 752
QY 714 WQQTUPTCEDPSGA-GVPRTLENVPLASPPKDEBDGASEENVVPVOLLQ 762
Db 753 WNTVGIINBDPGNCEGVKRTLSFSLRS---RVSGRHWKNFALVPLLR 798

RESULT 3
JC7531
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7531
R;Peng, J.B.; Chen, X.; Berger, U.V.; Weremowicz, S.; Morton, C.C.; Vassilev, P.M.; Bro
Biochem. Biophys. Res. Commun. 278, 326-332, 2000
A;Title: Human calcium transport protein Cat1.
A;Reference number: JC7531; MUID:20551480; PMID:11097838
A;Accession: JC7531
A;Molecule type: mRNA
A;Residues: 1-725 <PEN>
A;Cross-references: UNIPROT:Q9H296; GB:AF304463
C;Comment: This protein, a member of a family of Ca2+ channels, has a role in cellular
ine and kidney.
C;Genetics:
A;Gene: Cat1
A;Map position: 7q33-34
C;Keywords: calcium channel; calcium transport; intestine; kidney; transmembrane protein

Query Match 15.8%; Score 634; DB 2; Length 725;
Best Local Similarity 29.2%; Pred. No. 5.3e-41;
Matches 187; Conservative 115; Mismatches 243; Indels 96; Gaps 20;

QY 98 LSKTSKYLTDSEYTEGSTGKTCLMKAVLNKDGVNACILPLQLIDRDSGNPQPLVNAQCT 157
Db 61 LNKLLKYEDCKVHRRGAMGETALHTAA--LYDNLEAAVMVIM-----EAAPE-LVPEPMT 111
QY 158 DDYTRGHSALHTAIEKRSQCQVKLVVENGANYHARACGRFFQKQGTCTCFYFGEPLPLSLAA 217
Db 112 SELYEGQTALHTAVNNQNNLVALLARRASVSARATGTAFRRSPCNLIYFGEHPLSPFAA 171
QY 218 CTQKQWDVVSYLENPHQPASLQATDSQGNTVLHALVMTSDNSAENIALVTSYMDGLL--- 274
Db 172 CVNSEIIVRLLEH---GADIRAQDSLGNTVLHLIL-----QPNKTFACQMYNLLLSYD 223
```

224 GGDHL---KSLVLPNNQGLFPFKLAGVEGNIWMFOHLMQK-----RKHIQWTYGP 271
336 VRVSLYDLASVDSC--EENSVLIEIIAFHCKSPHRRHWVLEPLNKLLOAKWDLLIPKFFLN 394
272 LTTSLYDLTEIDSSGDDQSLLLEIV--TTKKREARQILDQTPVKVELVSLKW----KRYGRP 326
395 FLCNL-----IWMFTFAVAHVQPTLKKQAAHPHKAENVN----- 429
327 YFCVLGALYVLYIICFTMCVVCP-----LKPRITRNTRNPRDNTLMQOKLQEAIV 377
430 ----SMLLTGHILILGGIYLIVGQWYFRRHV--FWISFIDSFYELFLFOALLTVV 483
378 TPKDDRLVGLSVIGVAIILLVEIPDIFRLGVTRFFGQTILGGPFHVIITVAFMWLV 437
484 SOVLCFCLAIEWYLLPLVLSALVGNLNLLYTTRGFOHTGIYSWMIQKIURDLRLFLIYL 543
438 TWVRLTNNVDSGVWPMSPALVGCNVMYFARGFQMLGPFITMIQKMIFGDLMRFCWLMA 497
544 VPLFGFVALVSLSQEAWRPEAPTGNATESVQPMWEGQDEGNGAOYRGFLEASLELKF 603
498 VVILGFASAFYIIFQ-----TEDPDELGHFYDYPMALFTTFELP-L 537
604 TIGMCELAFQEQHLFRGMVLLLLLAFLVLLTYILLNMLIALMSETVNSVATDSWSWKQL 663
538 TIIDGPANYVDLDFP--MYSVTYAAFAIATILMLNLLIAMGDTWHRVAHERDELWRAQ 595
664 KAISVLEWNGY---WV-----CRKKQKQAGVMLTVGTKPDGSPDERWCFRVEE 708
596 VVATTWMLERKLPRCLWPFRSGICGREYGLG-----DRWFLRVED 634

RESULT 5
JC7795
epithelial calcium channel 1, ECaC1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
C:Accession: JC7795
R:Weber, K.; Erben, R.G.; Rump, A.; Adamski, J.
Biochem. Biophys. Res. Commun. 289, 1287-1294, 2001
A:Title: Gene structure and regulation of the murine epithelial calcium channels ECaC1
A:Reference number: JC7795
A:Accession: JC7795
A:Molecule type: DNA
A:Residues: 1-723 <WEB>
A:Cross-references: GB:AF336378
C:Comment: This calcium channel plays an important role in active transcellular calcium
relevant for in vivo calcium homeostasis.
C:Genetics:
A:Gene: ECaC1
A:Map position: 6
A:Introns: 3/72; 70/1; 111/1; 157/1; 190/1; 247/3; 296/3; 367/3; 422/2; 477/3; 5
C:Keywords: calcium channel

Query Match 14.5%; Score 581; DB 2; Length 723;
Best Local Similarity 26.8%; Pred. No. 6.9e-37;
Matches 191; Conservative 118; Mismatches 263; Indels 140; Gaps 25;

QY 113 GSTGKTCMLKAVLNKDGYNACILPLQLDRDSGNFQP-LVNAQCTDDYYRGHSALHAI 171
DB 70 GALGETALHVA--LYDNLDAAILM-----EAPYLVTESTLCEPFVGQTALHIV 119
QY 172 EKRSLOCVKLLVNGANVHARACGRFQKQGTCTFEGELPLSLAACTKQWDVVSYLLEN 231
DB 120 MNQNVNLRALLARGASARATGSAPHRSSHNLIIYGEHPHLSFPAACVSEEVRLLEIH 179
QY 232 PHOPASIQATDSQGNVTLHALVMSIDNSAENIALVTSWYDGLL--QAGARLCPTVQLEDI 289
DB 180 ---GADIRAQDSIGNVTLHLVL-----QNKTFACQMYNLLLSYDGDHL---KSLLEV 228
QY 290 RNLQDLTPKLAAKEGKIEIFRHILOREFSGLSHLRKFTWCYGPVRVSYLDLASVDSC 349
DB 229 PNNQGLTPFKLAGVEGNIWMFOHLMQK-----RKRIQWSFGPLTSSLYDLTEIDSW 279

QY 350 -BENSULEIAFHCKSPHRRHVVLE--PLNKLQAKWDLILPKPFLNFCML-----LY 401
 DB 280 GEELSLELVWSKKKEARQ---ILSQTPVKELVSLKW---KKYQOPYFCLLGALYIFY 332
 QY 402 MFIFTAVAHQOP-----TLKKQAAHPLKAEVGNMMLTGHIILGGIYL 446
 DB 333 MCVFTCCYRPLKFRDANRTHVRDNTIMEQSKLQEAITYYQDKIRLVGELVTIGAVII 392
 QY 447 L-----VGQLWYFRRHRHFWISFIDSYPEILFLFQALLTVVSVQVLCFLAIBWYLP 497
 DB 393 LLELEIPDIRVGASRYFGQ-----TVLGGPHVIIITVASVLLTMAURLTNNGEVV 445
 QY 498 LLVSALVGLWNLIIYTRGFQHTGIYSVMQKVLRLRLLIYLVFLFGFAVALVSLS 557
 DB 446 PMSMALVGLWCVMYFARGFQMLPPTIMQKIFGDLRFQWLMAMVILGFASAFYIIF 505
 QY 558 QEAWRPEATGPNATESVQPMQGEDEGNGAORYGLEASLELFKFTIGMGLAFOQLH 617
 DB 506 Q-----TEDPDLGFSFDPYPMFSTFELF-ITIIDGPANYRVDLP 545
 QY 618 FRGMVILLAYVLLFYILLNMLMSETVNSVATDSWSIWKLQAKAISVLEMENGYWM 677
 DB 546 F--MYSVTYATPAIIATLLMLNLFIAMMGDTHWRVAQERDELWRAQVWATTWMLE----- 598
 QY 678 CRXKQR-----AGVMLTVGTHKPGSDPDERKCFVEE-----VNWASW 714
 DB 599 -RMPRFLMPSRGICCEYGLG-----DRWLFVEHHQBNQYRVLYRYVEAFKSSDK 649
 QY 715 EOTLPTLCE-DPSGAGVPRTLE-NPVLASPPKDEDEGASEENVYPVQLLOSN 764
 DB 650 BEVQEQISEKQPSGTETGLARGSVVLQTPPLSRITSLSNSHRGWEILRN 701
 RESULT 6
 T33026
 hypothetical protein T09A12.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T33026
 R:Hawkins, J.; Fulton, B.; Gillam, B.
 submitted to the EMBL Data Library, February 1998
 A:Description: The sequence of C. elegans cosmid T09A12.
 A:Reference number: Z21265
 A:Accession: T33026
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-900 <HAW>
 A:Cross-references: UNIPROT:O61220; EMBL:AF047660; PIDN:AAC04431.1; GSPDB:GN000022; CESP:
 A:Experimental source: strain Bristol N2; clone T09A12
 C:Genetics:
 A:Gene: CESP:T09A12.3
 A:Map position: 4
 A:Introns: 43/2; 86/3; 260/2; 396/3; 424/2; 495/1; 517/3; 553/3; 691/3; 741/3; 780/3; 82
 Query Match 10.3%; Score 414; DB 2; Length 900;
 Best Local Similarity 24.2%; Pred. No. 8.6e-24;
 Matches 183; Conservative 113; Mismatches 253; Indels 206; Gaps 32;
 QY 61 RKTGASQDPNRRDRDLFNAVSRGVPEDLAFLPEYLSKTSKYL-----TDSEYTE 112
 DB 98 KKGKGS--GPNVLDD---FNQGENVGD-----LKKALKLLDGGKGGKGNESKYRE 144
 QY 113 -----GSTGKTCLMKAVLNKQGNACILPLQIDRDSGNPQPLVNAQCTDDYYRGH 164
 DB 145 ISWKLEERGSMGTIIIGCLLHASDTHNALVLKILDY-----YPKLNDIHISEDYF-GU 198
 QY 165 SALHIAIERSLQCVKLLVNGENAVHARACGRFF-----QKQGT----- 204
 DB 199 SPLHQAIINTDCKLVYKPLKGLGADVNSRCYGAFFCADDQKASRTDSLEHYVELSUKTNY 258
 QY 205 --CFYFGLPLSLAACTKQWDVVSYLLENPHQPASLQATDSQNTVVLHALVMI SDNSASN 262

DB 259 TGNMYLGEYPLSFAACLNPBESFRLLLAFLKAMP---NAQDTNGNSVLHMCVI-----HEN 310
 QY 263 IALVTSMDGLLOAGARLCPTVQLEDIRNLQDLTFLKLAKEGKIEIFRHILQRFSGLS 322
 DB 311 WA---MFKLALECCGASL-RTV-----NKQSLSPLLTAAKLAKKEMFDEILLEGDSV- 358
 QY 323 HLSRKFTWCVGPVRVSLYDLASVDSREN-----SVLEIIAFHCKSPHRRHVMVLEP 375
 DB 359 -----WAYGDASTAYPLAKITINETTGELNEASALSUVYGTQVHEHLELDGL-- 408
 QY 376 LNKLLQAKWDLILPK-FFLFLCNLIYMFIFTAV-----AYHQP-- 413
 DB 409 LDTLLEAKWEAPAKNMIVSFTAPTLYYICFVTAFTLRPIGFSTEMLTGEMINRYSEPPP 468
 QY 414 -----TLKKQAP-----HLKAEVGNMMLTGHIILGGIYLLV 448
 DB 469 GRYGNSTLQOVKPVINATSRGLVEWSEPLSQCHLRNWDPPDPFANSYIRLVFELFVI 528
 QY 449 GQLWYFRRHRHFWISFID-----SYFEILFLFOALLT-----VVSVLCLFLAIEW 494
 DB 529 GIC-----VOVFLQDRDIKRIKGRKWNVLTAFPKITTFLTYFLVLAIMPTRACDL 581
 QY 495 YLPLFLV-----SALVGLWNLIIYTRGFQHTGIYSVMQKVLRLRLLIYLVFLF 547
 DB 582 SPVLLVVDNVLITVTMTTHVLYYCRVIRFPVGPVLMVYTIATDIFRFLIYIGIFLM 641
 QY 548 GP--AVALVLSQEAWRPEATGPNATESVQPMQGEDE-----NGAQY 590
 DB 642 GFSQSFLIFLSC--REANVIKLLITDQSEASEGSDKNFNI.TROI SAYDTAIVKNAEYF 699
 QY 591 RGLSEASLELF--KFTIGMGLAFOQLHFRGMVL-----LILLAYVLLTYILL 637
 DB 700 ENVMOSPTEAFVTRTILTIQEPT-----VLYRMLALCPANTMVMWIKVVFILFELFVSI 755
 QY 638 LNMILMSETVNSVATDSWSIWKLQAKAISVLEME 672
 DB 756 FNMLIAMWTRIVETIFQGLE-YKQRAQVILMLE 789
 RESULT 7
 T33012
 hypothetical protein F28H7.10 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T20312; T21533
 R:Matthews, P.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: Z19255
 A:Accession: T20312
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-790 <WIL>
 A:Cross-references: UNIPROT:P90784; EMBL:Z74030; PIDN:CAA98449.1; GSPDB:GN000023; CESP:F2
 A:Experimental source: clone D1054
 R:Berts, M.
 submitted to the EMBL Data Library, May 1996
 A:Reference number: Z19435
 A:Accession: T21533
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-790 <W12>
 A:Cross-references: EMBL:Z72508; PIDN:CAA96644.1; GSPDB:GN000023; CESP:F28H7.10
 A:Experimental source: clone F28H7
 C:Genetics:
 A:Gene: CESP:F28H7.10
 A:Map position: 5
 A:Introns: 46/2; 89/3; 129/1; 157/1; 201/1; 264/2; 349/3; 406/3; 487/3; 543/2; 580/1; 67
 Query Match 9.8%; Score 392.5; DB 2; Length 790;
 Best Local Similarity 25.3%; Pred. No. 3.4e-22;
 Matches 182; Conservative 106; Mismatches 223; Indels 189; Gaps 35;
 QY 61 RKTGASQDP-PNRRDRDLFNAVSRGVPEDLAFLPEYLSKTSKYL-----TDSEY 111


```

QY 362 -CKSPH-----RHMVVL-----EPLAK-LLOAKWDL 387
Db 727 GCKSADEDEPKLEKDAQSASNDYRVKYHPLKLMADAELKHLNPLSKALLKYKNRL 786
QY 388 -IPKFFLNLFLNIYFIETAVAYHOPTL-----KKQAAPHLKAEVGN 430
Db 787 GRPMYFALPMVLVFIIVSLTQYVVRHTKAPYNVWNESSYDSEYFDENETCPQINTTKPD- 845
QY 431 MLTGTGHIILGIGIYLLVGLQWTFWRHVFI--WISFIDSYFILLFLQ-ALLTVVSQVL 487
Db 846 -VVMKIIQTLAVCOILVECFQFORKFAYLVNWNMID-----CFIYSTALITVYDFSE 899
QY 488 CF---LAIEMWPLLSVALVGLMNLVYTRGFQHTGYISVNIQKVILRDLRLFLLIYL 543
Db 900 CSATSGVRQWQWILALCIPFGWINLLFMIRKMPREGIFVVMFVIV-KTFFRFPFV 958
QY 544 VLFEGFAVALVSLSQEAWREAPT---GNPATESVQPMQEGDEGNGAQRGILEASLEL 600
Db 959 LFIATSSSFVILQN--REFSTIFMSPLKTTVM--MIGE----- 995
QY 601 FKFTIGMGEIAFOEQLHFRGN-----VLLLLAYVLLTYILLNMLIAMSETNSV 652
Db 996 FEFT--GIFHGDETHAERMGFGPAHTAVACALFFFFCIIMTILLMNLVGLAVDDIKGV 1052
QY 653 ATDSWSWTKLQKALS-VLEME-----NGY--WWCRKK 681
Db 1053 -QEKAEKLRLAMQVDLVLOIEASLSHPFIQTKKYATCRYATFPYKLUHKTGFAGWNSFR 1111
QY 682 QRAGVMLTVGTKPD 695
Db 1112 RRFQ--LSVSTDPE 1123

```

RESULT 12

```

JH0588
calmodulin-binding protein trpl - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
R;Phillips, A.M.; Bull, A.; Kelly, L.E.
C;Accession: JH0588
Neuron 8, 631-642, 1992
A;Title: Identification of a Drosophila gene encoding a calmodulin-binding protein with
A;Reference number: JH0588; MUID:92232293; PMID:1314616
A;Accession: JH0588
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1124 <PHI>
A;Cross-references: UNIPROT:P48994; GB:M88185; NID:g469057; PID:g158715
A;Experimental source: head
C;Genetics:
A;Gene: trpl
A;Cross-references: FlyBase:FBgn0005614
C;Superfamily: TRPC3 protein
C;Keywords: calmodulin binding; phosphoprotein; transmembrane protein
F;341-362/Domain: transmembrane #status predicted <TM1>
F;374-396/Domain: transmembrane #status predicted <TM2>
F;462-479/Domain: transmembrane #status predicted <TM3>
F;512-533/Domain: transmembrane #status predicted <TM4>
F;549-572/Domain: transmembrane #status predicted <TM5>
F;643-668/Domain: transmembrane #status predicted <TM6>
F;710-727,809-825/Region: calmodulin binding #status predicted
F;722/Binding site: phosphate (Ser) (covalent) #status predicted

```

```

Query Match 4.9%; Score 197.5; DB 2; Length 1124;
Best Local Similarity 19.7%; Pred. No. 7.6e-07;
Matches 162; Conservative 130; Mismatches 281; Indels 249; Gaps 38;

```

```

QY 131 VNACILPLQLIDRDSGNPQL-----VNAQCTDD 159
Db 25 VGGCCVPL-----GLPQPLLEBKFPFLAVERGDMPNVRRILQKALRHQINICWDP 77
QY 160 YRGHSALHIAIEKRSQCCKLLVNG-----ANVHARAC-----GRFFQKG 201

```

```

Db 78 L--GRRALTALNDENLEMVLLVMGVETKDALHAINABFVEAVELLLEHEELIYKGG 135
QY 202 Q-----GTCFYFGEI-PLSLAACTQWDVWSYLLEN-----PH-----OPASL 238
Db 136 EYYSQKQVDINTAMFADITPLMLAAHKNFILLRLLDRGAAPVPHDIRCCBECVRL 195
QY 239 QATDSQGNTVLH-----ALVMISDNSEALNTVSMYDGLGLOAGARLCPTVOLED 288
Db 196 TAEDSLRHSLSRVNIYRALSPLICTNSDPSSTAFQLSWELRNALTAQECKSEYMDL 255
QY 289 INNLQ-----DLTPLKAAKEGKIEI-----FRHILQRESEGLSHLSRKTEWC 332
Db 256 RRQCKQFAVDLLDQTRTSNELAIILNYPQMSYEPEDRMSLTRLVQALSYKQKKEV--A 313
QY 333 YGPVRVSL-----YDLASVDSCEENSYLEIIAFHCKSPHRRHVMVLEPLNKL-- 383
Db 314 HSNIQQLLSIWD--GLPGFRKSIQDKVI--CIA-----QVAVLFPLYCLIYMCAPNCR 365
QY 384 WDLILPKFFLNLFCN---LIYMFIFTAVA-----YHOPTLKQAAPHLKAEVGN 429
Db 366 TQQLMRKPPMKELIHASSYLLFFILLVSRADDDFVRIFGTTRMKKELAEQELRQRG 425
QY 430 SMLLTGHILILGGIYLLVGLQWYFRRHVFIWISFIDSYFEILFLFOALL--TVVSQVL 487
Db 426 ---TPSKLELIWVMYV---IGFVMEVQEIFAVGMKSYLRNMWNFIDFLRNSLYVSM 477
QY 488 CFLAIEW-----YLP-----LLVSALVGLMNLVLYTRGFQ 518
Db 478 CLRFAFYIOQATEIARDPQMAVYIPREKWHDDPQLTAAGLFAANVFSALKVHLPSINP 537
QY 519 HTGIYSVMIQKVIKILRDLRLFLTYLVLFQFAVALVSLSQEAW-----RPEAPTGNAT 572
Db 538 HLGPLQISLGRMVI-DIVKFFFIYTLVLFAPA---CGLNQLWYFAALEKSKCVLP-- 591
QY 573 ESVQPMQEGDENGA-----QYRGILEASLELKFPTIGMGEI-----AQEQLHFR 619
Db 592 -----GEADWGHGSDSCMKWRFRFQNLPESSQSLEWASFGVMGLDDFELSJKSYTRFW 644
QY 620 GMVLLALLAVLLTYILLNMLIAMSETNSVATDSWSIWKLOKAIISVLEMENGYWCCR 679
Db 645 G--LLMPGYSVINVLNLLIAMSNSYAMIDEHSDTEWKFAR-----TKLWMSY 694
QY 680 KKQAGVMLTVGTPKDGSDERWCFRV-----EYVNWASWQTLPCLTLC 722
Db 695 FEDSA---TLPPFNVLPVSKVIRFKSSKTTIDQRSKKRKEQEFSEYDINIMRSLV 750
QY 723 EDPSGAGVPTLENPVLASPPKDE--DGASENYVPVQLLQ 762
Db 751 W-RYVAAHMKRFEN---NPVSEDDINEVKSEINTMYEMLE 787

```

RESULT 13

```

JN0015
trp protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Feb-2001
C;Accession: JN0015
R;Wong, F.; Schaefer, E.L.; Roop, B.C.; LaMendola, J.N.; Johnson-Seaton, D.; Shao, D.
Neuron 3, 81-94, 1989
A;Title: Proper function of the Drosophila trp gene product during pupal development is
A;Reference number: JN0015; MUID:90148782; PMID:2482778
A;Accession: JN0015
A;Molecule type: mRNA
A;Residues: 1-1274 <WON>
C;Comment: This photoreceptor membrane-associated protein is not required for the occur
C;Genetics:
A;Gene: trp
A;Cross-references: FlyBase:FBgn0003861
A;Map position: 95C5-6
C;Superfamily: TRPC3 protein
C;Keywords: glycoprotein; nucleotide binding; P-loop; phosphoprotein; transmembrane pro
F;1257-1263/Region: nucleotide-binding motif A (P-loop)

```

F:64,70,899/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:191,602,880,883,924/Binding site: phosphate (Ser) (covalent) #status predicted
 F:800,1266/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 4.8%; Score 191; DB 2; Length 1274;
 Best Local Similarity 20.2%; Pred. No. 2.9e-06;
 Matches 134; Conservative 99; Mismatches 237; Indels 192; Gaps 30;

QY 153 NQAQCTDDYRGHSALHIAIEKRSLOCVKLLVNGANVHARACGRFFQKGQGTCTFFGELP 212
 DB 62 NINCTDPNMR--SALISAENENFDMVILLENHIEV-----GDALLHAISEY 108

QY 213 LSLAACKQWDVVSYLEPHOPASLOQATDSQNT-----VLHALVMSNSAENIALVTS 268
 DB 109 VEAVEBELLQWEETNH---KEGQPSWEAVDRSKSTFTVDITPLILAAHRNNYILKI--- 162

QY 269 MYDGLLOAGARL-----CPTVQLED-----IRNLQDLTLPKLAKEG 305
 DB 163 ----LLDRGATLPMHDVKCGDECVTSQTDSLRHSQSRINAYRALSASSIALSSRP 218

QY 306 KIBIFRHILQREFSGLSHRKFTWCYGPVRVSLYDLAS--VDSCEENSVLBIIFPHCK 363
 DB 219 VLTAFO--LSWELKRLQAMESEFRAE-YTEMQVMQDFGTSLLDHARTSMELEVMLNFH 275

QY 364 SP-----HRRMVVLEP-LNKLLQAKWDLIPKF----- 391
 DB 276 EPSHDIWCLASSETLERLKLAIYKQKTFVAHPNVQQLAAIHWYDGLPGFPQASQQLMD 335

QY 392 FLNFCNLNLYMFIFTAVAHQPTLKKQAAPHLK-AEVGNSMLLTG-----HILILL 441
 DB 336 VVKLGCSFPPIY-----SLKYLAPDSEGAKFMRNPLSSSRPTCSYMPFLMLL 383

QY 442 GGYLLVGLQ-----WYF-----WRRH-----VF----- 460
 DB 384 GAASLRVQITPELLAPPWMLTMDWRKHGSLPGPIELAIITYMALIPEELKSLYS 443

QY 461 -----IW--ISPIDSYPILFLP--QALLTVVSQVLCFLAIEWYL-----PL 498
 DB 444 DGLFEYIMDLNNTVDYISNMFYVTILCRATAWIVHRLWFRGIDPYPREHWHFDDPM 503

QY 499 LVS-----ALVGLMNLNLYYTRGFQHTGIYSVMIOKVILRDLRLFLLYLVFLGFAVA 552
 DB 504 LLESGAPAGMVSFLKLVHIFINPHLGLQVSLGRMII-DIIKFFIYTLVLFAPG-- 560

QY 553 LVLSQEAQMPREAPTPGNATESVQPMGEDEGNGA-----QYRGILEASLELFKFTIGM 607
 DB 561 -CGLNQLLWY-YAELEKNKCYHLHPDVADPDFDQEKACTIWRREFSNLFTSQSLFASFG 618

QY 608 GELAFQ-----QLHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIKLQ 663
 DB 619 VDLVSPDLAGIKSFTFRFWALLMFGYSVINIIVLLNMLIAMMSNSYQIISERADTEWKA 678

QY 664 KA 665
 DB 679 RS 680

RESULT 14
 JU0092
 trp protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 17-Nov-2000
 C:Accession: JU0092
 R:Montell, C.; Rubin, G.M.
 Neuron 2, 1313-1323, 1989
 A:Title: Molecular characterization of the Drosophila trp locus: a putative integral mem
 A:Reference number: JU0092; MUID:90180449; PMID:2516726
 A:Accession: JU0092
 A:Molecule type: mRNA
 A:Residues: 1-1275 <MON>
 A:Experimental source: strain Oregon R
 C:Comment: trp protein is expressed predominantly in the rhabdomic membranes of the ph
 C:Genetics:

A:Gene: trp
 A:Cross-references: FlyBase:FBgn0003861
 C:Superfamily: TRP3 protein
 C:Keywords: transmembrane protein

F:334-354/Domain: transmembrane #status predicted <TM1>
 F:378-401/Domain: transmembrane #status predicted <TM2>
 F:419-436/Domain: transmembrane #status predicted <TM3>
 F:457-477/Domain: transmembrane #status predicted <TM4>
 F:504-527/Domain: transmembrane #status predicted <TM5>
 F:612-630/Domain: transmembrane #status predicted <TM6>
 F:636-661/Domain: transmembrane #status predicted <TM7>

Query Match 4.8%; Score 190.5; DB 2; Length 1275;
 Best Local Similarity 19.9%; Pred. No. 3.1e-06;
 Matches 130; Conservative 98; Mismatches 253; Indels 171; Gaps 27;

QY 153 NQAQCTDDYRGHSALHIAIEKRSLOCVKLLVNGANVHARACGRFFQKGQGTCTFFGELP 212
 DB 62 NINCTDPNMR--SALISAENENFDMVILLENHIEV-----GDALLHAISEY 108

QY 213 LSLAACKQWDVVSYLEPHOPASLOQATDSQNTV---LHALVMSNSAENIALVTS 269
 DB 109 VEAVEBELLQWEETNH---KEGQPSWEAVDRSKSTFTVDITPLILAAHRNNYILKI--- 162

QY 270 YDGLLOAGARL-----CPTVQLED-----IRNLQDLTLPKLAKEG 306
 DB 163 ----LLDRGATLPMHDVKCGDECVTSQTDSLRHSQSRINAYRALSASSIALSSRPV 219

QY 307 IBIFRHILQREFSGLSHRKFTWCYGPVRVSLYDLAS--VDSCEENSVLBIIFPHCKS 364
 DB 220 LTAFO--LSWELKRLQAMESEFRAE-YTEMQVMQDFGTSLLDHARTSMELEVMLNFHE 276

QY 365 P-----HRRMVVLEP-LNKLLQAKWDLIPKF----- 391
 DB 277 PSHDIWCLGQRTLERLKLAIYKQKTFVAHPNVQQLAAIHWYDGLPGFRKQASQQLMD 336

QY 392 FLNFCNLNLYMFIFTAVAHQPTLKKQAAPHLKAEVNSMLLTGHLIILLGGIYLLVGLQ 451
 DB 337 VVKLGCSFPPIYSLKYLAPDSEGAKFMRKPFVKPFIHSCSYN--PFLMLLGAASLRVQI 394

QY 452 -----WYF-----WRRH-----VF-----I 461
 DB 395 TPELLAPPWMLTMDWRKHGSLPGPIELAIITYMALIPEELKSLYSDGLFEYIMDL 454

QY 462 W--ISPIDSYPILFLP--QALLTVVSQVLCFLAIEWYL-----PLIYS-----A 502
 DB 455 MNVIDYISNMFYVTILCRATAWIVHRLWFRGIDPYPREHWHFDDPMLISEGAFAG 514

QY 503 LVGLMNLNLYYTRGFQHTGIYSVMIOKVILRDLRLFLLYLVFLGFVALVLSQEA 562
 DB 515 MVSFLKLVHIFINPHLGLQVSLGRMII-DIIKFFIYTLVLFAPG--CGLNQLLWY 570

QY 563 PEAPTPGNATESVQPMGEDEGNGA-----QYRGILEASLELFKFTIGMELAFQ--- 614
 DB 571 -YAELEKNKCYHLHPDVADPDFDQEKACTIWRREFSNLFTSQSLFASFGVLDVSPDLA 629

QY 615 -QLHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIKLQKA 665
 DB 630 IKSFTFRFWALLMFGYSVINIIVLLNMLIAMMSNSYQIISERADTEWKFARS 681

RESULT 15
 I38361
 TRPC1 protein - human
 C:Species: Homo sapiens (man)
 C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 04-Sep-1998
 C:Accession: I38361
 R:Wes, P.D.; Chevesich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, C.
 Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995
 A:Title: TRPC1, a human homolog of a Drosophila store-operated channel.
 A:Reference number: I38361; MUID:96003837; PMID:7568191
 A:Accession: I38361
 A>Status: preliminary; translated from GB/EMBL/DBJ

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2005, 11:12:14 ; Search time 165 Seconds
(without alignments)
1790.818 Million cell updates/sec

Title: US-09-445-614B-2
Perfect score: 4004.
Sequence: 1 MTPSSSPVRLTLGGQE.....EEDGASENYVPVQLQSN 764

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4004	100.0	764	2 AAY29469	Aay29469 Human van
2	4004	100.0	764	2 AAY06559	Aay06559 Human van
3	4004	100.0	764	3 AAY97358	Aay97358 Human VR-
4	4004	100.0	764	4 AAB35622	Aab35622 Human van
5	4004	100.0	764	5 AAM51859	Aam51859 Human van
6	4004	100.0	764	5 ABB07817	Abb07817 Human van
7	4004	100.0	764	6 ABU04099	Abu04099 Human exp
8	4004	100.0	764	6 ABU04113	Abu04113 Human exp
9	4004	100.0	764	6 ABU04095	Abu04095 Human exp
10	4004	100.0	764	6 ABU04104	Abu04104 Human exp
11	4004	100.0	764	6 ABU04110	Abu04110 Human exp
12	4004	100.0	764	6 ABU04106	Abu04106 Human exp
13	4004	100.0	764	6 ABU04096	Abu04096 Human exp
14	4004	100.0	764	8 ADI81598	Adi81598 Human van
15	4004	100.0	764	8 ADP66663	Adp66663 Human van
16	4004	100.0	764	8 ADQ89074	Adq89074 Human uro
17	4004	100.0	764	8 ADP25061	Adp25061 PRO polyp
18	3998	99.9	764	4 AAE04890	Aae04890 Human tra
19	3998	99.9	764	4 AAE01230	Aae01230 Human van
20	3998	99.9	764	6 ABU04101	Abu04101 Human exp
21	3998	99.9	764	6 ABU04100	Abu04100 Human exp
22	3988.5	99.6	763	2 AAY29471	Aay29471 Human van
23	3988.5	99.6	763	2 AAY42308	Aay42308 Human van
24	3988.5	99.6	763	6 ABU04107	Abu04107 Human exp
25	3988.5	99.6	763	6 ABU04098	Abu04098 Human exp

26	3988.5	99.6	763	6 ABU04108	Abu04108 Human exp
27	3988.5	99.6	889	5 ABG99067	Abg99067 Human van
28	3988.5	99.6	889	6 ABO42807	Abo42807 Human van
29	3945	98.5	764	5 AAM51860	Aam51860 Human van
30	3945	98.5	764	5 ABB07818	Abb07818 Human van
31	3945	98.5	764	6 ABU04112	Abu04112 Human exp
32	3945	98.5	764	6 ABU04097	Abu04097 Human exp
33	3945	98.5	764	6 ABU04114	Abu04114 Human exp
34	3945	98.5	764	8 ADP181600	Adp181600 Human van
35	3945	98.5	764	8 ADP09701	Adp09701 Human VRL
36	3939	98.4	764	3 AAY84834	Aay84834 Amino aci
37	3939	98.4	764	6 ABU04109	Abu04109 Human exp
38	3375	84.3	644	8 ADI81574	Adi81574 Human van
39	3258	81.4	630	3 AAY97364	Aay97364 Human VR-
40	3258	81.4	630	6 ABU04111	Abu04111 Human exp
41	3159	78.9	756	8 ADI81616	Adi81616 Mouse gro
42	3158	78.9	756	8 ADI81582	Adi81582 Mouse gro
43	3051.5	76.2	761	2 AAY06556	Aay06556 Rat vanil
44	3051.5	76.2	761	2 AAW99790	Aaw99790 Rat VRRP-
45	3051.5	76.2	761	8 ADI81576	Adi81576 Rat vanil

ALIGNMENTS

RESULT 1
AAY29469
ID AAY29469 standard; protein; 764 AA.
XX
AC AAY29469;
XX
DT 08-OCT-1999 (first entry)
XX
DE Human vanilloid receptor homologue VANILREP2.
XX
KW Human; vanilloid receptor homologue; VANILREP2; polymorphic variant;
KW PVP-1; therapy; diagnosis; chronic pain; neuropathic; postoperative;
KW rheumatoid arthritis; neuralgia; algesia; nerve injury; ischaemia;
KW neurodegeneration; stroke; incontinence; inflammatory disorder.
XX
OS Homo sapiens.
XX
FN WO9937765-A1.
XX
PD 29-JUL-1999.
XX
PF 25-JAN-1999; 99WO-EP000420.
XX
PR 27-JAN-1998; 98EP-00300549.
PR 26-OCT-1998; 98GB-00023421.
PR 20-JAN-1999; 99GB-00001209.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Davis JB, Duckworth DM, Hayes PD;
XX
DR WPI; 1999-479049/40.
XX
DR N-PSDB; AAZ07114.
XX
FT New human vanilloid receptor homologues (VANILREP2).
XX
PS Claim 4; Page 30-32; 47pp; English.
XX
CC The present sequence represents a human vanilloid receptor homologue,
CC designated VANILREP2. VANILREP2 can be used to diagnose disease or
CC susceptibility to disease related to expression or activity of VANILREP2
CC polypeptides. VANILREP2 may be used to treat diseases including pain,
CC (for example chronic, neuropathic, postoperative, rheumatoid arthritis),
CC neuralgia, algesia, nerve injury, ischaemia, neurodegeneration, stroke,
CC incontinence, and inflammatory disorders
XX
SQ Sequence 764 AA;

Query Match	100.0%;	Score 4004;	DB 2;	Length 764;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 764;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	MTSPSSPVRL	ETLDGGQDGEADRGKLD	FGSGLPPMESQFGEDRKFAFQIRVNLNY 60	
DB	1	MTSPSSPVRL	ETLDGGQDGEADRGKLD	FGSGLPPMESQFGEDRKFAFQIRVNLNY 60	
QY	61	RKGTGASQDP	PNRFDRLFN	AVSRGVPEDL	AGLPEYLSKYLTDSEYTGSGTKTCL 120
DB	61	RKGTGASQDP	PNRFDRLFN	AVSRGVPEDL	AGLPEYLSKYLTDSEYTGSGTKTCL 120
QY	121	MKAVLNKDGV	NACILPLLIQIDRDSGN	POPLVNAOCTDDYYRGHSALHIAIEKRSIQCVK 180	
DB	121	MKAVLNKDGV	NACILPLLIQIDRDSGN	POPLVNAOCTDDYYRGHSALHIAIEKRSIQCVK 180	
QY	181	LLVENGANV	HARACGRFFQKGQCTCFY	FGELPLSLAACTKQWDVSYLLENPHQPASLOA 240	
DB	181	LLVENGANV	HARACGRFFQKGQCTCFY	FGELPLSLAACTKQWDVSYLLENPHQPASLOA 240	
QY	241	TDSQGNVTL	HALVMI	SDNSAENIALVTSMYDGLLOAGARLCPTVQLEDIRNLQDLTPKL 300	
DB	241	TDSQGNVTL	HALVMI	SDNSAENIALVTSMYDGLLOAGARLCPTVQLEDIRNLQDLTPKL 300	
QY	301	AAKEGKIEI	FRHILOREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIAF 360		
DB	301	AAKEGKIEI	FRHILOREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIAF 360		
QY	361	HCKSPHRRM	VVLEPLNKLQAKWDL	LIPKFFLNFLCNLIYMFIFTAVAYHQTLLKQAA 420	
DB	361	HCKSPHRRM	VVLEPLNKLQAKWDL	LIPKFFLNFLCNLIYMFIFTAVAYHQTLLKQAA 420	
QY	421	PHLKAEGVNS	MLTGHITLILGGIYLLVGOLWYFWRHVFIMISFIDSFEILFLFOALL 480		
DB	421	PHLKAEGVNS	MLTGHITLILGGIYLLVGOLWYFWRHVFIMISFIDSFEILFLFOALL 480		
QY	481	TVVSQVLCFL	AEIEMWYLP	LVLSALVGLWNLVYTRGFQHTGIYSVMIQVILRDILRFL 540	
DB	481	TVVSQVLCFL	AEIEMWYLP	LVLSALVGLWNLVYTRGFQHTGIYSVMIQVILRDILRFL 540	
QY	541	IYLVFLFGFA	VALVLSQEA	RPEAPTGNPNATESVQFMGEQDEGNGAQYRGILEASLEL 600	
DB	541	IYLVFLFGFA	VALVLSQEA	RPEAPTGNPNATESVQFMGEQDEGNGAQYRGILEASLEL 600	
QY	601	FKFTIGMGE	LAFOQLHFRGMVLLIILAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660		
DB	601	FKFTIGMGE	LAFOQLHFRGMVLLIILAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660		
QY	661	KLOKAISVLE	MENGYWCRKKQAGV	MLTVGTPDGS	PDERWCFRVEEYNWASWEQTLPT 720
DB	661	KLOKAISVLE	MENGYWCRKKQAGV	MLTVGTPDGS	PDERWCFRVEEYNWASWEQTLPT 720
QY	721	LCBDSGAGV	PTLENPVLASPPKDEDEGASEENYVPVQLQSN 764		
DB	721	LCBDSGAGV	PTLENPVLASPPKDEDEGASEENYVPVQLQSN 764		

RESULT 2
AA06559
ID AAY06559 standard; protein; 764 AA.
XX
AC AAY06559;
XX
XX
DT 08-OCT-1999 (first entry)
XX
DE Human vanilloid receptor-related polypeptide 1 (VRRP-1).
XX
XX Vanilloid receptor-related polypeptide 1; VRRP-1; VR2;
XX capsaicin receptor; VR1; human; vanilloid; analgesic; pain; inflammation;
XX therapy; diagnosis.
XX
OS Homo sapiens.
XX

PN	W09937675-A1.
XX	
PD	29-JUL-1999.
XX	
PF	22-JAN-1999; 99WO-US001418.
XX	
PR	22-JAN-1998; 98US-0072151P.
XX	
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Julius DJ, Caterina M, Brake AJ;
XX	
DR	WPI; 1999-469113/39.
XX	
DR	N-PSDB; AAX87492.
XX	
PT	New isolated capsaicin receptor polypeptide and related nucleic acid -
PT	useful for detecting vanilloid compounds, identifying modulators, and in
PT	diagnosis or treatment of e.g. pain and inflammation.
XX	
PS	Claim 4; Page 110-112; 120pp; English.
XX	
CC	The present sequence represents human vanilloid receptor-related
CC	polypeptide 1 (VRRP-1 or VR2), as deduced from a cDNA clone (see
CC	AAX87492) isolated from human CCRF-CEM cells. VRRP-1 is an example of a
CC	capsaicin receptor-related polypeptide of the invention. It is not
CC	activated by capsaicin or heat, but may interact with the novel capsaicin
CC	receptor VR1 (see AAY06558). The invention provides vanilloid receptor
CC	polypeptides and polynucleotides, including capsaicin receptor-related
CC	polypeptides and polynucleotides, as well as expression vectors, host
CC	cells and transgenic animals. It also provides a method of using such
CC	receptors to identify vanilloid compounds in natural products or to
CC	screen candidate compounds that modulate capsaicin receptor function for
CC	use as analgesics (vanilloid analogues, therapeutic antibodies, antisense
CC	oligonucleotides, capsaicin receptor-encoding polynucleotides for gene
CC	therapy), flavour-enhancing agents, etc. Capsaicin receptor-related
CC	polypeptides and specific antibodies can also be used for the diagnosis
CC	and treatment of human disease and pain
XX	
SQ	Sequence 764 AA;

Query Match		100.0%;	Score 4004;	DB 2;	Length 764;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 764;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MTSPSSPVRLTLDGGQDGEADRGKLD	FGSGLPPMESQFGEDRKFAFQIRVNLNY	60	
DB	1	MTSPSSPVRLTLDGGQDGEADRGKLD	FGSGLPPMESQFGEDRKFAFQIRVNLNY	60	
QY	61	RKGTGASQDPNRFDRDLFNAVSRGV	PEDLAGLPEYLSKYLTDSEYTGSGTKTCL	120	
DB	61	RKGTGASQDPNRFDRDLFNAVSRGV	PEDLAGLPEYLSKYLTDSEYTGSGTKTCL	120	
QY	121	MKAVLNKDGVNACILPLLIQIDRDSGN	POPLVNAOCTDDYYRGHSALHIAIEKRSIQCVK	180	
DB	121	MKAVLNKDGVNACILPLLIQIDRDSGN	POPLVNAOCTDDYYRGHSALHIAIEKRSIQCVK	180	
QY	181	LLVENGANVHARACGRFFQKGQCTCFY	FGELPLSLAACTKQWDVSYLLENPHQPASLOA	240	
DB	181	LLVENGANVHARACGRFFQKGQCTCFY	FGELPLSLAACTKQWDVSYLLENPHQPASLOA	240	
QY	241	TDSQGNVTLHALVMI	SDNSAENIALVTSMYDGLLOAGARLCPTVQLEDIRNLQDLTPKL	300	
DB	241	TDSQGNVTLHALVMI	SDNSAENIALVTSMYDGLLOAGARLCPTVQLEDIRNLQDLTPKL	300	
QY	301	AAKEGKIEIFRHILOREFSGLSHL	SRKFTWCYGPVRVSLYDLASVDSCEENSVLIIAF	360	
DB	301	AAKEGKIEIFRHILOREFSGLSHL	SRKFTWCYGPVRVSLYDLASVDSCEENSVLIIAF	360	
QY	361	HCKSPHRRMVLEPLNKLQAKWDL	LIPKFFLNFLCNLIYMFIFTAVAYHQTLLKQAA	420	
DB	361	HCKSPHRRMVLEPLNKLQAKWDL	LIPKFFLNFLCNLIYMFIFTAVAYHQTLLKQAA	420	
QY	421	PHLKAEGVNSMLTGHILILGGIYLL	VGQLWYFWRHVFIMISFIDSFEILFLFOALL	480	

Db	421	PHLKAIEVGNMLTGHILLLGGYLLVGLQWYFMRHHVFIWISPDYSYFEILFLFOALL	480
Qy	481	TVVSQVLCFLAIIEWYLPPLVLSALVGLWNLNLYYTRGFQHTGYYSVMIOKVILRDLRFL	540
Db	481	TVVSQVLCFLAIIEWYLPPLVLSALVGLWNLNLYYTRGFQHTGYYSVMIOKVILRDLRFL	540
Qy	541	IYLVFLPGFAVALVLSQEARPEAPTGNATESVQPMGEQDEGNGAQRGTLASLEL	600
Db	541	IYLVFLPGFAVALVLSQEARPEAPTGNATESVQPMGEQDEGNGAQRGTLASLEL	600
Qy	601	FKFTIGMGLAFOELHFRGMVLLLLAYVLLFYILLNMLIALMSETVNSVATDSWSIW	660
Db	601	FKFTIGMGLAFOELHFRGMVLLLLAYVLLFYILLNMLIALMSETVNSVATDSWSIW	660
Qy	661	KLOKAI SVLEMENGYWCRKQKQAGVWLTVTGTPDGSPOBRWCPRVEEYNWASWEQTLP	720
Db	661	KLOKAI SVLEMENGYWCRKQKQAGVWLTVTGTPDGSPOBRWCPRVEEYNWASWEQTLP	720
Qy	721	LCEDPSGAGVPRTELPVLSPPKEDGEGASEENYVPVQLQSN	764
Db	721	LCEDPSGAGVPRTELPVLSPPKEDGEGASEENYVPVQLQSN	764
RESULT 3			
AA97358			
ID	AA97358 standard; protein; 764 AA.		
XX			
AC	AA97358;		
XX			
DT	05-SEP-2000 (first entry)		
XX			
DE	Human VR-2 protein.		
XX			
KW	VR-2; human; vanilloid receptor; nociceptor; pain signalling;		
KW	hyperalgesia; musculoskeletal disorder; neuropathic pain;		
KW	chromosome 17p11-12; gene therapy.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
Modified-site	2..5	/note= "cGMP-dependent protein kinase phosphorylation site"	
Domain	162..194	/label= ankyrin_repeat_domain	
Modified-site	169..174	/note= "myristoylation site"	
Modified-site	171..174	/note= "N-glycosylation site"	
Modified-site	192..195	/note= "N-glycosylation site"	
Domain	208..243	/label= ankyrin_repeat_domain	
Domain	293..328	/label= ankyrin_repeat_domain	
Modified-site	368..375	/note= "tyrosine kinase phosphorylation site"	
Modified-site	368..371	/note= "cGMP-dependent protein kinase phosphorylation site"	
Domain	391..410	/label= transmembrane_domain	
Domain	431..448	/label= transmembrane_domain	
Domain	459..476	/label= transmembrane_domain	
Domain	486..508	/label= transmembrane_domain	
Modified-site	499..502	/note= "cGMP-dependent protein kinase phosphorylation site"	
Domain	538..556		

FT	Modified-site	/label= transmembrane_domain	
FT		604..607	
FT	Domain	/note= "N-glycosylation site"	
FT		621..645	
FT	Modified-site	/label= transmembrane_domain	
FT		622..628	
FT	Modified-site	/note= "tyrosine kinase phosphorylation site"	
FT		749..752	
FT	Modified-site	/note= "N-glycosylation site"	
FT		765..770	
FT		/note= "myristoylation site"	
XX			
PN	WO200029577-A1.		
XX			
PD	25-MAY-2000.		
XX			
PP	12-NOV-1999;	99WO-US026701.	
XX			
PR	13-NOV-1998;	98US-0108322P.	
PR	28-DEC-1998;	98US-0114078P.	
PR	26-FEB-1999;	99US-00258633.	
PR	19-OCT-1999;	99US-00421134.	
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Curtis RAJ;		
XX			
DR	WPI; 2000-387790/33.		
DR	N-PSDB; AAA30254.		
XX			
XX	New capsaicin/vanilloid receptor polynucleotides and polypeptides, used to modulate pain signaling mechanisms.		
PT			
PT			
PS	Claim 11; Fig 2; 183pp; English.		
PS			
XX			
CC	The present sequence is the protein sequence for human capsaicin/vanilloid receptor VR-2, which is involved in pain signalling. The coding sequence was isolated by searching a heart cDNA library for genes encoding novel receptors of the capsaicin/vanilloid family, and has been shown to be located at chromosome 17p11-12. This region has been associated with myasthenia gravis, Smith-Magenis syndrome, CORD5, Cone-rod dystrophy, choroidal dystrophy, central areolar and retinal cone dystrophy, and it is possible that the protein may be used to treat or diagnose these disorders. In addition, the gene, protein and its antibodies can be used to diagnose and treat hyperalgesia, inflammation, infection, ischaemia, joint pain, tooth pain, headaches, pain associated with surgery or neuropathic pain, possibly via the use of gene therapy		
CC			
CC			
CC			
CC			
CC			
CC			
CC			
CC			
CC			
CC			
CC			
CC			
CC			
XX			
XX			
SQ	Sequence 764 AA;		
	Query Match	100.0%;	Score 4004; DB 3; Length 764;
	Best Local Similarity	100.0%;	Pred. NO. 0;
	Matches	764;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MTSPSSSPVFRLETLDGQGDSEADRGKLDPGSLPPMESQFGEDRKFAPIQIRVNLNY	60
Db	1	MTSPSSSPVFRLETLDGQGDSEADRGKLDPGSLPPMESQFGEDRKFAPIQIRVNLNY	60
QY	61	RKGTGASQDPNPRFDRDLFNVAISRGVPEDLAGLPEYLSKYLTDSEYTGSTGKTCL	120
Db	61	RKGTGASQDPNPRFDRDLFNVAISRGVPEDLAGLPEYLSKYLTDSEYTGSTGKTCL	120
QY	121	MKAVNLKQGVNACILPQLQIDRDSGNPQPLVNAQCTDDYVRGSHALHIAIEKRSLOCVK	180
Db	121	MKAVNLKQGVNACILPQLQIDRDSGNPQPLVNAQCTDDYVRGSHALHIAIEKRSLOCVK	180
QY	181	LLVENGANVHARACGRFFQKQCTCFYFGBELPLSLAACTKQWDVVSVYLLNPHOPASLQA	240
Db	181	LLVENGANVHARACGRFFQKQCTCFYFGBELPLSLAACTKQWDVVSVYLLNPHOPASLQA	240
QY	241	TDSQGNVTLHALVMSIDNSAENIALVTSMDGLLQAGARLCPTVQLEDIRNLQDLTPKL	300
Db	241	TDSQGNVTLHALVMSIDNSAENIALVTSMDGLLQAGARLCPTVQLEDIRNLQDLTPKL	300

QY 301 AAKEGKIEIFRHILOREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIF 360
DB 301 AAKEGKIEIFRHILOREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIF 360
QY 361 HCKSPHRHVMVLEPLNKLQAKWDLILPKFFLNFLCNLIYMFIFTAVAYHQTLLKQAA 420
DB 361 HCKSPHRHVMVLEPLNKLQAKWDLILPKFFLNFLCNLIYMFIFTAVAYHQTLLKQAA 420
QY 421 PHLKAEVGNMMLTGHIILLLGGIYLLVQGLWYFMRHVFIIWISFIDSIFEILFLFQALL 480
DB 421 PHLKAEVGNMMLTGHIILLLGGIYLLVQGLWYFMRHVFIIWISFIDSIFEILFLFQALL 480
QY 481 TVVSQVLCFLAIEWYLPLLSALVGLWNLIIYTRGFQHTGIYSVMIQVILRDLRLFL 540
DB 481 TVVSQVLCFLAIEWYLPLLSALVGLWNLIIYTRGFQHTGIYSVMIQVILRDLRLFL 540
QY 541 IYLVFLFGFAVALVSIQSEAWRPEAPTPGNATESVQPMGEQDEGNGAQRGILEASLEL 600
DB 541 IYLVFLFGFAVALVSIQSEAWRPEAPTPGNATESVQPMGEQDEGNGAQRGILEASLEL 600
QY 601 FKFTIGMGLAFQEQHLHFRGMVLLLLAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660
DB 601 FKFTIGMGLAFQEQHLHFRGMVLLLLAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAI SVLEMENGYWCRKKQKQAGVMLTVGTYPDGS PDERWCPRVEEVNWNASWEQTLP 720
DB 661 KLOKAI SVLEMENGYWCRKKQKQAGVMLTVGTYPDGS PDERWCPRVEEVNWNASWEQTLP 720
QY 721 LCEDPSGAGVPRTPLENPVLASPPKDEDEGASEENYVPVQLQSN 764
DB 721 LCEDPSGAGVPRTPLENPVLASPPKDEDEGASEENYVPVQLQSN 764

RESULT 4
AAB35622
ID AAB35622 standard; protein; 764 AA.
XX AAB35622;
DT 14-FEB-2001 (first entry)
XX Human vanilloid receptor like receptor protein.
DE
XX VR-L; vanilloid receptor-like receptor; pain; infection; allergy;
KW mechanical injury; lymphoid tissue; human.
XX Homo sapiens.
XX GB2346882-A.
XX 23-AUG-2000.
XX 02-DEC-1999; 99GB-00028566.
XX 08-DEC-1998; 98GB-00027016.
XX (MERI) MERCK SHARP & DOHME LTD.
PA Bonnert TP;
PI
XX WPI; 2001-064250/08.
DR N-PSDB; AAC60297.
XX New polynucleotide encoding human vanilloid receptor-like receptor for
PT diagnosing and treating pain, infections, allergies, and cancers.
XX Claim 1; Fig 1; 36pp; English.
XX The present invention relates to the human vanilloid receptor-like
CC receptor. This receptor may be used for diagnosing or treating conditions
CC associated with altered vanilloid receptor-like (VR-L) receptor
CC expression. It may also be used to treat abnormal conditions associated

CC with pain. Conditions or diseases that can be diagnosed or treated
CC include viral, bacterial and fungal infections, allergic responses,
CC mechanical injury associated with trauma, hereditary diseases, lymphoma
CC or carcinoma, or other conditions which activate the genes of the
CC lymphoid tissues
XX
SQ Sequence 764 AA;
Query Match 100.0%; Score 4004; DB 4; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPSSSPVFRLETDGGQDGEADRGKLDGSGLPWMEQFQGEDRKFAPOIRVNLNY 60
DB 1 MTPSSSPVFRLETDGGQDGEADRGKLDGSGLPWMEQFQGEDRKFAPOIRVNLNY 60
QY 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSGTKCL 120
DB 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSGTKCL 120
QY 121 MKAVNLKDGVNACILPLLQIDRDSGNPOPLVNAOCTDDYGRGHSALHIAIEKRSIQCVK 180
DB 121 MKAVNLKDGVNACILPLLQIDRDSGNPOPLVNAOCTDDYGRGHSALHIAIEKRSIQCVK 180
QY 181 LLVENGANVHABACGRFFQKGGTCTFYGELPLSLAACTKOWDVVSYLLENPHOPASLOA 240
DB 181 LLVENGANVHABACGRFFQKGGTCTFYGELPLSLAACTKOWDVVSYLLENPHOPASLOA 240
QY 241 TDSQNTVHLHALVMI SDNSAENIALVTSMYDGLQAGARLCPTVQLEDIRNLQDLTPKL 300
DB 241 TDSQNTVHLHALVMI SDNSAENIALVTSMYDGLQAGARLCPTVQLEDIRNLQDLTPKL 300
QY 301 AAKEGKIEIFRHILOREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIF 360
DB 301 AAKEGKIEIFRHILOREFSGLSHLSRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIF 360
QY 361 HCKSPHRHVMVLEPLNKLQAKWDLILPKFFLNFLCNLIYMFIFTAVAYHQTLLKQAA 420
DB 361 HCKSPHRHVMVLEPLNKLQAKWDLILPKFFLNFLCNLIYMFIFTAVAYHQTLLKQAA 420
QY 421 PHLKAEVGNMMLTGHIILLLGGIYLLVQGLWYFMRHVFIIWISFIDSIFEILFLFQALL 480
DB 421 PHLKAEVGNMMLTGHIILLLGGIYLLVQGLWYFMRHVFIIWISFIDSIFEILFLFQALL 480
QY 481 TVVSQVLCFLAIEWYLPLLSALVGLWNLIIYTRGFQHTGIYSVMIQVILRDLRLFL 540
DB 481 TVVSQVLCFLAIEWYLPLLSALVGLWNLIIYTRGFQHTGIYSVMIQVILRDLRLFL 540
QY 541 IYLVFLFGFAVALVSIQSEAWRPEAPTPGNATESVQPMGEQDEGNGAQRGILEASLEL 600
DB 541 IYLVFLFGFAVALVSIQSEAWRPEAPTPGNATESVQPMGEQDEGNGAQRGILEASLEL 600
QY 601 FKFTIGMGLAFQEQHLHFRGMVLLLLAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660
DB 601 FKFTIGMGLAFQEQHLHFRGMVLLLLAYVLLTYIILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKAI SVLEMENGYWCRKKQKQAGVMLTVGTYPDGS PDERWCPRVEEVNWNASWEQTLP 720
DB 661 KLOKAI SVLEMENGYWCRKKQKQAGVMLTVGTYPDGS PDERWCPRVEEVNWNASWEQTLP 720
QY 721 LCEDPSGAGVPRTPLENPVLASPPKDEDEGASEENYVPVQLQSN 764
DB 721 LCEDPSGAGVPRTPLENPVLASPPKDEDEGASEENYVPVQLQSN 764
RESULT 5
AAM51859
ID AAM51859 standard; protein; 764 AA.
XX
AC AAM51859;
XX
DT 29-JAN-2002 (first entry)
XX

DE Human vanilloid receptor 1.
 XX Human; TLCC-2; TRP-like calcium channel; membrane excitability;
 KW nociception; nootropic; neuroprotective; antiparkinsonian; cycostatic;
 KW hypotensive; antidepressant; analgesic; anticonvulsant; tranquiliser;
 KW Parkinson's disease; Huntington's disease; multiple sclerosis;
 KW Gilles de la Tourette's syndrome; autonomic function disorder; cancer;
 KW neuroleptic; gene therapy; Alzheimer's disease; CNS disorder.
 XX Homo sapiens.
 OS WO200177331-A1.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-US011442.
 XX 07-APR-2000; 2000US-00544797.
 XX (MILL-) MILLENIUM PHARM INC.
 XX Curtis RAJ, Silos-Santiago I;
 XX WPI; 2002-010913/01.
 XX Novel isolated human transient receptor potential-like calcium channel
 PT protein-2 useful for treating Alzheimer's disease, depression, amnesia,
 PT pain disorder, and cancer.
 XX Example 1; Page 131-134; 148pp; English.
 XX The present invention relates to the protein and coding sequences of
 CC human transient receptor potential (TRP)-like calcium channel protein-2
 CC (TLCC-2). The sequences can be used in the treatment of TLCC-2 related
 CC disorders, including central nervous system disorders such as
 CC Alzheimer's, Parkinson's and Huntington's diseases, multiple sclerosis,
 CC Gilles de la Tourette's syndrome, autonomic function disorders, learning
 CC or memory disorders, pain disorders and disorders of cellular
 CC proliferation, including cancer. The present sequence is the human
 CC vanilloid receptor 1 which was described in the exemplification of the
 CC invention
 XX Sequence 764 AA;
 SQ

Query Match 100.0%; Score 4004; DB 5; Length 764;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPSSSPVPLETLDDGGQDSEADRGKLDGSGLPPEMESQFQGEDRKEFAPQIRVNLY 60
 DB 1 MTPSSSPVPLETLDDGGQDSEADRGKLDGSGLPPEMESQFQGEDRKEFAPQIRVNLY 60
 QY 61 RKGTGASQPDNRDRDLFNAVRGVPEDLAGLPEYLSKTSKYLTDSYETEGSTGKTCL 120
 DB 61 RKGTGASQPDNRDRDLFNAVRGVPEDLAGLPEYLSKTSKYLTDSYETEGSTGKTCL 120
 QY 121 MKAVLNKDGYNACILPLQLIDRDSGNPQPLVNAQCTDDYRGHSAHIAIEKRSLOCVK 180
 DB 121 MKAVLNKDGYNACILPLQLIDRDSGNPQPLVNAQCTDDYRGHSAHIAIEKRSLOCVK 180
 QY 181 LLVENGANVHARACGRPFQKGGTCFYRGLPELSIACTKQDWVSVYLLNPHOPASLOA 240
 DB 181 LLVENGANVHARACGRPFQKGGTCFYRGLPELSIACTKQDWVSVYLLNPHOPASLOA 240
 QY 241 TDSQNTVHLVMI SDSAENIALVTSMYDGLLQAGARLCTTVQLEDIRNLQDLTPKL 300
 DB 241 TDSQNTVHLVMI SDSAENIALVTSMYDGLLQAGARLCTTVQLEDIRNLQDLTPKL 300
 QY 301 AAKEGKIEIFRHILQREFSGLSLRSKFTWCYGPVRVSLVDLASVDSCEANSVLEIAF 360
 DB 301 AAKEGKIEIFRHILQREFSGLSLRSKFTWCYGPVRVSLVDLASVDSCEANSVLEIAF 360
 QY 361 HCKSPHRHVMVLEPLNKLQAKWDLIPKFFLNFLCNLIYFIPTAVAHQPTLKKQAA 420

DB 361 HCKSPHRHVMVLEPLNKLQAKWDLIPKFFLNFLCNLIYFIPTAVAHQPTLKKQAA 420
 QY 421 PHLKAEGVNSMLLTGHIILGGLYLLGQWYFRRHVFIWISFIDSFEILFLFOALL 480
 DB 421 PHLKAEGVNSMLLTGHIILGGLYLLGQWYFRRHVFIWISFIDSFEILFLFOALL 480
 QY 481 TVVSQVLCFLALEWYLPPLVLSALVGLWNLNLLYTRGFQHTGIYSVMIQVILRDLRFL 540
 DB 481 TVVSQVLCFLALEWYLPPLVLSALVGLWNLNLLYTRGFQHTGIYSVMIQVILRDLRFL 540
 QY 541 IYLVFLPGFAVALVSLSQEAWRPEAPTGNATESVQPMEGDEGNGAQRGLASLEL 600
 DB 541 IYLVFLPGFAVALVSLSQEAWRPEAPTGNATESVQPMEGDEGNGAQRGLASLEL 600
 QY 601 FKFTTGMGELAFQEQHFRGMVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660
 DB 601 FKFTTGMGELAFQEQHFRGMVLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660
 QY 661 KLQKAI SVLEMENGYWCRKQKQAGVMTVGTGPDGSPDERMCFRVEEVNWSWEQTLPT 720
 DB 661 KLQKAI SVLEMENGYWCRKQKQAGVMTVGTGPDGSPDERMCFRVEEVNWSWEQTLPT 720
 QY 721 LCEDPSGAGVPRTLENPVLASPPKEDGASEENYVPVQLQSN 764
 DB 721 LCEDPSGAGVPRTLENPVLASPPKEDGASEENYVPVQLQSN 764

RESULT 6
 ABB07817
 ID ABB07817 standard; protein; 764 AA.
 XX
 AC ABB07817;
 XX
 DT 03-JUL-2002 (first entry)
 XX
 DE Human vanilloid receptor 1.
 XX
 KW Transient receptor potential like calcium channel; TRP; TLCC-2; human;
 KW neuroprotective; analgesic; nootropic; antiparkinsonian; antidepressant;
 KW cerebroprotective; anxiolytic; antimanic; anticonvulsant; gene therapy;
 KW calcium signaling; vanilloid receptor 1.
 XX
 OS Homo sapiens.
 XX
 XX US2002035056-A1.
 XX
 XX 21-MAR-2002.
 XX
 XX 06-APR-2001; 2001US-00828466.
 XX
 XX 07-APR-2000; 2000US-00544797.
 XX
 XX (CURT/) CURTIS R A J.
 XX (SILO/) SILOS-SANTIAGO I.
 XX
 XX Curtis RAJ, Silos-Santiago I;
 XX WPI; 2002-338931/37.
 XX
 XX New nucleic acid designated TLCC-2 encodes a transient receptor potential
 PT -like calcium channel and is useful to diagnose and treat pain disorders
 PT and central nervous system neurodegenerative and neurological disorders.
 XX
 XX Disclosure; Fig 6; 70pp; English.
 XX
 XX The invention relates to a novel transient receptor potential (TRP)-like
 CC calcium channel, designated TLCC-2 and polynucleotides encoding the TLCC-
 CC 2. TLCC-2 can be expressed by standard recombinant methodology. The TLCC-
 CC 2 polypeptide, polynucleotides and modulators are useful for treating
 CC central nervous system disorders such as neurodegenerative disorders for
 CC example Alzheimer's disease, Parkinson's disease, multiple sclerosis,
 CC amyotrophic lateral sclerosis, progressive supranuclear palsy, epilepsy,

CC Creutzfeldt-Jakob disease, AIDS-related dementia, familial infantile
CC convulsions, paroxysmal choreoathetosis, psychiatric disorders such as
CC depression, anxiety, schizophrenia, psychoses, mania or phobic disorders,
CC learning or memory disorders such as amnesia, age-related memory loss, or
CC a neurological disorder such as migraine. The molecules are also useful
CC to treat a pain disorder. The present sequence represents a human
CC vanilloid receptor 1, used in alignment studies with the rVLC-2
CC polypeptide
XX
SQ Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 5; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSPVFRLETLDDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFAPIRVNLNY 60
Db 1 MTSPPSPVFRLETLDDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFAPIRVNLNY 60
QY 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTEGSTGKTCL 120
Db 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTEGSTGKTCL 120
QY 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRSHSAHIAIKRSIQCVK 180
Db 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRSHSAHIAIKRSIQCVK 180
QY 181 LLVENGANVHARACGRFFQKQGCTCFYFGBELPLSLAACTQMDVSVYLLNPHQASLOA 240
Db 181 LLVENGANVHARACGRFFQKQGCTCFYFGBELPLSLAACTQMDVSVYLLNPHQASLOA 240
QY 241 TDSQGNVTLHALVMSDNSAENTALTSMYDGLLOAGARLCPVQLIEDIRNLDLTPKL 300
Db 241 TDSQGNVTLHALVMSDNSAENTALTSMYDGLLOAGARLCPVQLIEDIRNLDLTPKL 300
QY 301 AAKEGKIEIPRHILQREFSGLSHRKFTWCYGPVRVSLYDLASVDSCEENSVLRIIF 360
Db 301 AAKEGKIEIPRHILQREFSGLSHRKFTWCYGPVRVSLYDLASVDSCEENSVLRIIF 360
QY 361 HCKSPHRRMVLEPLNKLQAKWDLIPKFFLNFLCNLIYMFIFTAVAYHPTLKKQAA 420
Db 361 HCKSPHRRMVLEPLNKLQAKWDLIPKFFLNFLCNLIYMFIFTAVAYHPTLKKQAA 420
QY 421 PHLKAEGVSNMLTGHILILGGIYLLVQQLWTFWRRHVPIWISPTDSYFEILFLQALL 480
Db 421 PHLKAEGVSNMLTGHILILGGIYLLVQQLWTFWRRHVPIWISPTDSYFEILFLQALL 480
QY 481 TVVSQVLCLAIIEWYLPVLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRDILRFL 540
Db 481 TVVSQVLCLAIIEWYLPVLSALVGLWNLNLYYTRGFQHTGIYSVMIQVILRDILRFL 540
QY 541 IYLVFLFGFAVALVLSQEAWRPEAPTGPNNATESVQPMQEDGNGAQYRGILEASLEL 600
Db 541 IYLVFLFGFAVALVLSQEAWRPEAPTGPNNATESVQPMQEDGNGAQYRGILEASLEL 600
QY 601 FKFTIGMELAFQELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
Db 601 FKFTIGMELAFQELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKALSIVLEMENGYWCRKKQAGVNLTVGTRKPDGSDPBRWCFRVEEVNWSWEGTLPT 720
Db 661 KLOKALSIVLEMENGYWCRKKQAGVNLTVGTRKPDGSDPBRWCFRVEEVNWSWEGTLPT 720
QY 721 LCDPDSGAGVPRTLNPVLSPPKDEDDGASEENYVPVQLQSN 764
Db 721 LCDPDSGAGVPRTLNPVLSPPKDEDDGASEENYVPVQLQSN 764

RESULT 7
ABU04099
ID ABU04099
XX
AC ABU04099;

XX 29-JAN-2003 (first entry)
XX Human expressed protein tag (EPT) #765.
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX Homo sapiens.
XX WO200278524-A2.
XX 10-OCT-2002.
XX 28-MAR-2002; 2002WO-US009671.
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0359985P.
XX (ZYCO-) ZYCOS INC.
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX Example 2; SEQ ID NO 765; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

Sequence 764 AA;
Query Match 100.0%; Score 4004; DB 6; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSPVFRLETLDDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFAPIRVNLNY 60
Db 1 MTSPPSPVFRLETLDDGGQEDGSEADRGKLDGSGLPMPMESQFGEDRKFAPIRVNLNY 60
QY 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTEGSTGKTCL 120
Db 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSEYTEGSTGKTCL 120
QY 121 MKAVLNKDGVNACILPLLIQIDRDSGNPQPLVNAOCTDDYRSHSAHIAIKRSIQCVK 180
XX

Db 121 MKAVNLKDGVNACILPLQLIDRDGSGNPQPLVNAQCTDDYRSGHSAHIAIEKRSLQCCKV 180
Qy 181 LLVENGANVHARACGRFFQKGQCTCFYFGLPLSLAACTKQWDVSVYLLNPHOPASLOA 240
Db 181 LLVENGANVHARACGRFFQKGQCTCFYFGLPLSLAACTKQWDVSVYLLNPHOPASLOA 240
Qy 241 TDSQGNVTLHALVWISDNSAENIALVTSMYDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300
Db 241 TDSQGNVTLHALVWISDNSAENIALVTSMYDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300
Qy 301 AAKEGKIEIFRHILQREFSGLSHLNRKFTWCYGPVRVSLYDLASVDSCEENSVEIIF 360
Db 301 AAKEGKIEIFRHILQREFSGLSHLNRKFTWCYGPVRVSLYDLASVDSCEENSVEIIF 360
Qy 361 HCKSPHRRMVLEPLNKLQAKWDLIIPKFELNLCNLIYMFIFTAVAHQPTLKKQAA 420
Db 361 HCKSPHRRMVLEPLNKLQAKWDLIIPKFELNLCNLIYMFIFTAVAHQPTLKKQAA 420
Qy 421 PHLKAEGVNSMLLTGHILILGGLYLLVQGLWYFRRHVFIIWISFIDSFEIIFLFOALL 480
Db 421 PHLKAEGVNSMLLTGHILILGGLYLLVQGLWYFRRHVFIIWISFIDSFEIIFLFOALL 480
Qy 481 TVVSQVLCFLAIEWYLPVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVLRLDLRFL 540
Db 481 TVVSQVLCFLAIEWYLPVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVLRLDLRFL 540
Qy 541 IYVFLRGPVALVSLQEAWRPEAPTPGNATSVQPMQEGDEGCAQYRGILEASLEL 600
Db 541 IYVFLRGPVALVSLQEAWRPEAPTPGNATSVQPMQEGDEGCAQYRGILEASLEL 600
Qy 601 FKFTIGMELAFQSLFRGMVLLIAYVLLTVILLNMLIAMSSTVNSVATDSWSIW 660
Db 601 FKFTIGMELAFQSLFRGMVLLIAYVLLTVILLNMLIAMSSTVNSVATDSWSIW 660
Qy 661 KLOKAISVLEMEYMWCRKKQKQAGVMTVGTGKPDGSPDERWCPRVEEVNWSWEQTLPT 720
Db 661 KLOKAISVLEMEYMWCRKKQKQAGVMTVGTGKPDGSPDERWCPRVEEVNWSWEQTLPT 720
Qy 721 LCEPDGAGVPRTLNVPVLSAPPKEDGASEENYVPVQLQSN 764
Db 721 LCEPDGAGVPRTLNVPVLSAPPKEDGASEENYVPVQLQSN 764

RESULT 8

ABU04113
ID ABU04113 standard; protein; 764 AA.

AC ABU04113;

XX 29-JAN-2003 (first entry)

DT Human expressed protein tag (BPT) #779.

DE Translational profiling; expressed protein tag; BPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

OS WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.
PA Chicz RM, Tomlinson AJ, Urban RG;
PI WPI; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX Example 2; SEQ ID NO 779; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: this sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 764 AA;
SQ

Query Match 100.0%; Score 4004; DB 6; Length 764;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSPPSSPVFRLETLTLDGGQDGEADRGKLDGSGLPMPMESQFGEDRKEAPQIRVNLNY 60
Db 1 MTSPPSSPVFRLETLTLDGGQDGEADRGKLDGSGLPMPMESQFGEDRKEAPQIRVNLNY 60
Qy 61 RKGTGASQDPNRFDRDLRFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
Db 61 RKGTGASQDPNRFDRDLRFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120
Qy 121 MKAVNLKDGVNACILPLQLIDRDGSGNPQPLVNAQCTDDYRSGHSAHIAIEKRSLQCCKV 180
Db 121 MKAVNLKDGVNACILPLQLIDRDGSGNPQPLVNAQCTDDYRSGHSAHIAIEKRSLQCCKV 180
Qy 181 LLVENGANVHARACGRFFQKGQCTCFYFGLPLSLAACTKQWDVSVYLLNPHOPASLOA 240
Db 181 LLVENGANVHARACGRFFQKGQCTCFYFGLPLSLAACTKQWDVSVYLLNPHOPASLOA 240
Qy 241 TDSQGNVTLHALVWISDNSAENIALVTSMYDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300
Db 241 TDSQGNVTLHALVWISDNSAENIALVTSMYDGLLQAGARLCTPTVQLEDIRNLQDLTPLKL 300
Qy 301 AAKEGKIEIFRHILQREFSGLSHLNRKFTWCYGPVRVSLYDLASVDSCEENSVEIIF 360
Db 301 AAKEGKIEIFRHILQREFSGLSHLNRKFTWCYGPVRVSLYDLASVDSCEENSVEIIF 360
Qy 361 HCKSPHRRMVLEPLNKLQAKWDLIIPKFELNLCNLIYMFIFTAVAHQPTLKKQAA 420
Db 361 HCKSPHRRMVLEPLNKLQAKWDLIIPKFELNLCNLIYMFIFTAVAHQPTLKKQAA 420
Qy 421 PHLKAEGVNSMLLTGHILILGGLYLLVQGLWYFRRHVFIIWISFIDSFEIIFLFOALL 480
Db 421 PHLKAEGVNSMLLTGHILILGGLYLLVQGLWYFRRHVFIIWISFIDSFEIIFLFOALL 480
Qy 481 TVVSQVLCFLAIEWYLPVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVLRLDLRFL 540
Db 481 TVVSQVLCFLAIEWYLPVLSALVGLWNLNLYYTRGFQHTGIYSVMIQKVLRLDLRFL 540

QY 541 IYLVFLGFAVALVSLQEARPPATGPNATESVQPMQDEGNGAQYRGILEASLEL 600
DB 541 IYLVFLGFAVALVSLQEARPPATGPNATESVQPMQDEGNGAQYRGILEASLEL 600
QY 601 FKFTIGMGLAFQEQHFRGMVLLIAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
DB 601 FKFTIGMGLAFQEQHFRGMVLLIAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLQKAISVLEMGYVWCRKQKQAGVNLTVGTPKDGSPDERWCFRVEEVNWSWQTLPT 720
DB 661 KLQKAISVLEMGYVWCRKQKQAGVNLTVGTPKDGSPDERWCFRVEEVNWSWQTLPT 720
QY 721 LCEDPSGAGVPRTLENPVLASPKDEDEGASEENYVPVQLQSN 764
DB 721 LCEDPSGAGVPRTLENPVLASPKDEDEGASEENYVPVQLQSN 764

RESULT 9
ID ABU04095
AC ABU04095;
XX
XX
DT 29-JAN-2003 (first entry)
XX Human expressed protein tag (EPT) #761.
DE
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX
XX 21-MAY-2001; 2001US-0292544P.
XX
XX 08-AUG-2001; 2001US-0310801P.
XX
XX 01-OCT-2001; 2001US-0326370P.
XX
XX 04-DEC-2001; 2001US-0336780P.
XX
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 761; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 6; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPSSSPVFRLETLDDGGQDGEADRGKLDGSGGLPMEQFOQEDRKFAPOIRVNLNY 60
DB 1 MTPSSSPVFRLETLDDGGQDGEADRGKLDGSGGLPMEQFOQEDRKFAPOIRVNLNY 60
QY 61 RKGTGASQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSKTCL 120
DB 61 RKGTGASQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSKTCL 120
QY 121 MKAVLNLDGYNACILPLLIQIDRDSGNPOPLVNAOCTDDYGRGHSALHIAIEKRSIQCVK 180
DB 121 MKAVLNLDGYNACILPLLIQIDRDSGNPOPLVNAOCTDDYGRGHSALHIAIEKRSIQCVK 180
QY 181 LLVENGANVHARACGRFFQKGQGTCTFYFGEPLSLAACTKQWDVVSYLENPHQASLOA 240
DB 181 LLVENGANVHARACGRFFQKGQGTCTFYFGEPLSLAACTKQWDVVSYLENPHQASLOA 240
QY 241 TDSQGNTVLHALVMTSDNSAENIALVTSMDGLLOAGARLCPTVQLEDIRNLQDLTPLKL 300
DB 241 TDSQGNTVLHALVMTSDNSAENIALVTSMDGLLOAGARLCPTVQLEDIRNLQDLTPLKL 300
QY 301 AAKEGKIETFRHILQREFSGLSHRKFTWCYGPVRSVLYDLASVDSCEENSVELEIAF 360
DB 301 AAKEGKIETFRHILQREFSGLSHRKFTWCYGPVRSVLYDLASVDSCEENSVELEIAF 360
QY 361 HCKSPHRHVMVLEPLNKLQAKWDLIPKPFNFCNLINFIETAVAYHPTLKKQAA 420
DB 361 HCKSPHRHVMVLEPLNKLQAKWDLIPKPFNFCNLINFIETAVAYHPTLKKQAA 420
QY 421 PHLKAEVGNMMLTGHILILIGGIYLLVGQLMYFWRHVFIMISFIDSYFELLFQALL 480
DB 421 PHLKAEVGNMMLTGHILILIGGIYLLVGQLMYFWRHVFIMISFIDSYFELLFQALL 480
QY 481 TVVSQVLCFLAIEWYLLPLVLSALVIGWNLNLLYYTRGFQHTGIYSVMIQKVIIRDLLRFL 540
DB 481 TVVSQVLCFLAIEWYLLPLVLSALVIGWNLNLLYYTRGFQHTGIYSVMIQKVIIRDLLRFL 540
QY 541 IYLVFLGFAVALVSLQEARPPATGPNATESVQPMQDEGNGAQYRGILEASLEL 600
DB 541 IYLVFLGFAVALVSLQEARPPATGPNATESVQPMQDEGNGAQYRGILEASLEL 600
QY 601 FKFTIGMGLAFQEQHFRGMVLLIAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
DB 601 FKFTIGMGLAFQEQHFRGMVLLIAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLQKAISVLEMGYVWCRKQKQAGVNLTVGTPKDGSPDERWCFRVEEVNWSWQTLPT 720
DB 661 KLQKAISVLEMGYVWCRKQKQAGVNLTVGTPKDGSPDERWCFRVEEVNWSWQTLPT 720
QY 721 LCEDPSGAGVPRTLENPVLASPKDEDEGASEENYVPVQLQSN 764
DB 721 LCEDPSGAGVPRTLENPVLASPKDEDEGASEENYVPVQLQSN 764

RESULT 10
ABU04104
ID ABU04104 standard; protein; 764 AA.
XX AC ABU04104;
XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #770.
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX OS Homo sapiens.
 XX PN WO200278524-A2.
 XX PD 10-OCT-2002.
 XX PF 28-MAR-2002; 2002WO-US009671.
 XX PR 28-MAR-2001; 2001US-0279495P.
 XX PR 21-MAY-2001; 2001US-0292544P.
 XX PR 08-AUG-2001; 2001US-0310801P.
 XX PR 01-OCT-2001; 2001US-0326370P.
 XX PR 04-DEC-2001; 2001US-0336780P.
 XX PR 20-FEB-2002; 2002US-0358985P.
 XX PA (ZYCO-) ZYCOS INC.
 XX PI Chicz RM, Tomlinson AJ, Urban RG;
 XX WPI; 2003-040607/03.
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX Example 2; SEQ ID NO 770; 134pp; English.
 XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIFO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 764 AA;
 SQ
 Query Match 100.0%; Score 4004; DB 6; Length 764;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTSPPSSPVFRLETLDDGGQDGESEADRGKLPFGSLPPMESQFQGEDRKFPQIRVNLNY 60
 DB 1 MTSPPSSPVFRLETLDDGGQDGESEADRGKLPFGSLPPMESQFQGEDRKFPQIRVNLNY 60
 QY 61 RKGTCASQPDNRPDRDLFNAVSRGVPEDLAAGLPEYLSKTSKYLTDSYEGSTGKTCL 120
 DB 61 RKGTCASQPDNRPDRDLFNAVSRGVPEDLAAGLPEYLSKTSKYLTDSYEGSTGKTCL 120
 QY 121 MKAVLNLDKGVNACILPLLIQDRDSDGNPQPLVNAQCTDDYYRGHSALHIAIEKSLQCVK 180
 DB 121 MKAVLNLDKGVNACILPLLIQDRDSDGNPQPLVNAQCTDDYYRGHSALHIAIEKSLQCVK 180

QY 181 LLVENGANVHARACGRFFQKGGTCTFYFGELPLSLAACTKQWDVVSYLENHPHQPASLOA 240
 DB 181 LLVENGANVHARACGRFFQKGGTCTFYFGELPLSLAACTKQWDVVSYLENHPHQPASLOA 240
 QY 241 TDSQGNVTLHALVMSISDAENIALVTSYDGLLQAGARLCPVQLQEDIRNLQDLTPKL 300
 DB 241 TDSQGNVTLHALVMSISDAENIALVTSYDGLLQAGARLCPVQLQEDIRNLQDLTPKL 300
 QY 301 AAKEGKIEIFRILQREFSGLSHLKFTWCYGPVRSYLYDIASVDSCEENSVLRIIAF 360
 DB 301 AAKEGKIEIFRILQREFSGLSHLKFTWCYGPVRSYLYDIASVDSCEENSVLRIIAF 360
 QY 361 HCKSPHRHMVLEPLNKLQAKWDLIIKPFNLFLCNLIYMFIFTAVAYHQPTLKKQAA 420
 DB 361 HCKSPHRHMVLEPLNKLQAKWDLIIKPFNLFLCNLIYMFIFTAVAYHQPTLKKQAA 420
 QY 421 PHLKAEVGNMILLTGHIILGLGIIYLLVGLMFWRRHVPIMISFIDSIFEILFLQALL 480
 DB 421 PHLKAEVGNMILLTGHIILGLGIIYLLVGLMFWRRHVPIMISFIDSIFEILFLQALL 480
 QY 481 TVVSQVLCFLAIEWLPLLVLSALVGLWMLLYYTRGFQHTGIYSVMIQKVLRLDLRFL 540
 DB 481 TVVSQVLCFLAIEWLPLLVLSALVGLWMLLYYTRGFQHTGIYSVMIQKVLRLDLRFL 540
 QY 541 IYLVFLGFAVALVLSQEAWRPEAPTGNATESVQPMQEGDEGNGAQYRGILEASLEL 600
 DB 541 IYLVFLGFAVALVLSQEAWRPEAPTGNATESVQPMQEGDEGNGAQYRGILEASLEL 600
 QY 601 FKFTIGMGLAFOELHFRGMVLLIILAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
 DB 601 FKFTIGMGLAFOELHFRGMVLLIILAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
 QY 661 KLOKALSVLEMENGYWCKKQKQAGVMTVGTGKDPGSDRWCFRVEEVNWSWEQTLPT 720
 DB 661 KLOKALSVLEMENGYWCKKQKQAGVMTVGTGKDPGSDRWCFRVEEVNWSWEQTLPT 720
 QY 721 LCDPDSGAGVPRTPLENPVLASPPKEDGSEENYVPVQLQSN 764
 DB 721 LCDPDSGAGVPRTPLENPVLASPPKEDGSEENYVPVQLQSN 764
 RESULT 11
 ABU04110
 ID ABU04110 standard; protein; 764 AA.
 AC ABU04110;
 XX 29-JAN-2003 (first entry)
 DT Human expressed protein tag (EPT) #776.
 DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX OS Homo sapiens.
 XX PN WO200278524-A2.
 XX PD 10-OCT-2002.
 XX PF 28-MAR-2002; 2002WO-US009671.
 XX PR 28-MAR-2001; 2001US-0279495P.
 XX PR 21-MAY-2001; 2001US-0292544P.
 XX PR 08-AUG-2001; 2001US-0310801P.
 XX PR 01-OCT-2001; 2001US-0326370P.
 XX PR 04-DEC-2001; 2001US-0336780P.
 XX PR 20-FEB-2002; 2002US-0358985P.
 XX PA (ZYCO-) ZYCOS INC.

XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 776; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 6; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSPPSPVRLTLDGGQDSEADRGKLDGSGLPMPESQFGEDRKFPAPQIRVNLNY 60
DB 1 MTSPPSPVRLTLDGGQDSEADRGKLDGSGLPMPESQFGEDRKFPAPQIRVNLNY 60

QY 61 RKTGASQDPNFRDRDLFNASVSGVPEDLAGLPEVLSKTSKYLTDSEYTESGKTCL 120
DB 61 RKTGASQDPNFRDRDLFNASVSGVPEDLAGLPEVLSKTSKYLTDSEYTESGKTCL 120

QY 121 MKAVLNKGVNACILPQLQIDRDSGNPQPLVNAQCTDDYVYRGSHALHIAEKRSIQCVK 180
DB 121 MKAVLNKGVNACILPQLQIDRDSGNPQPLVNAQCTDDYVYRGSHALHIAEKRSIQCVK 180

QY 181 LLVENGANVHARACGRPFQKQGTCTFVFGELPLSLAACTKQWDVSVLLENPHQASLOA 240
DB 181 LLVENGANVHARACGRPFQKQGTCTFVFGELPLSLAACTKQWDVSVLLENPHQASLOA 240

QY 241 TDSQGNVTLHALVMSDNSAENIALVTSMDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300
DB 241 TDSQGNVTLHALVMSDNSAENIALVTSMDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300

QY 301 AAKEGKTEIPRHLQREFSGLSHLNRKFTWCYGPVRSVLYDLASVDSCEENSVLBIAP 360
DB 301 AAKEGKTEIPRHLQREFSGLSHLNRKFTWCYGPVRSVLYDLASVDSCEENSVLBIAP 360

QY 361 HCKSPHRHVMVLEPLNKLQAKWDLIPKFFNELCNLYMETFTAVAVHOPTLAKQAA 420
DB 361 HCKSPHRHVMVLEPLNKLQAKWDLIPKFFNELCNLYMETFTAVAVHOPTLAKQAA 420

QY 421 PHLKAEGVNSMLTGHILLLGGIYLLVQGLWTFWRHVFVWISFSDSYEILFLFQALL 480
DB 421 PHLKAEGVNSMLTGHILLLGGIYLLVQGLWTFWRHVFVWISFSDSYEILFLFQALL 480

QY 481 TVVSQVLCFLAIEWYLPPLVSALVGLWNLNLYYTRGPHQHTGIYSVMIQVILRDLRFL 540
DB 481 TVVSQVLCFLAIEWYLPPLVSALVGLWNLNLYYTRGPHQHTGIYSVMIQVILRDLRFL 540

QY 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMQEGDEGNGAQYRGILEASLEL 600

DB 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMQEGDEGNGAQYRGILEASLEL 600
QY 601 FKFTTGMGELAFQEQHFRGMVLLLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660
DB 601 FKFTTGMGELAFQEQHFRGMVLLLLLLAYVLLTYILLNMLTALMSETVNSVATDSWSIW 660
QY 661 KLOKAISVLEMGYWMCKKQKORAGVMLTVGTPKDGSPDERWCERFVEEVNWSWQTLPT 720
DB 661 KLOKAISVLEMGYWMCKKQKORAGVMLTVGTPKDGSPDERWCERFVEEVNWSWQTLPT 720
QY 721 LCEDPSGAGVPRTELENPNVLASPPKEDDEGCASENYPVQLQSN 764
DB 721 LCEDPSGAGVPRTELENPNVLASPPKEDDEGCASENYPVQLQSN 764

RESULT 12
ABU04106
ID ABU04106 standard; protein; 764 AA.
XX ABU04106;
XX
XX 29-JAN-2003 (first entry)
XX Human expressed protein tag (EPT) #772.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
XX
XX Chicz RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX
XX Example 2; SEQ ID NO 772; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 6; Length 764;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSFSSPVFRLETLGGQDGEADRGKLDGSGLPMPMESQFGEDRKFPQIRVNLNY 60
 DB 1 MTSFSSPVFRLETLGGQDGEADRGKLDGSGLPMPMESQFGEDRKFPQIRVNLNY 60

QY 61 RKTGASQDPNFRDRDLNFAVSRGVPEDLAGLPEYLSKTYLTDSEYESTGKTCL 120
 DB 61 RKTGASQDPNFRDRDLNFAVSRGVPEDLAGLPEYLSKTYLTDSEYESTGKTCL 120

QY 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGSALHIAIEKRSQCCKV 180
 DB 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGSALHIAIEKRSQCCKV 180

QY 181 LKAVENGANVHARACGRFFQKQGTCTFYFGBELPLSLAACTKQWDVSVYLLNPHQASLOA 240
 DB 181 LKAVENGANVHARACGRFFQKQGTCTFYFGBELPLSLAACTKQWDVSVYLLNPHQASLOA 240

QY 241 TDSQNTVLHALVMSNSAENIALVTSMYDGLQAGARLCPTVQLEDIRNLDLTPKL 300
 DB 241 TDSQNTVLHALVMSNSAENIALVTSMYDGLQAGARLCPTVQLEDIRNLDLTPKL 300

QY 301 AAKGKTEIPRHILQREFSGLSHLSKFTWCYGVRSVLYDLASVDSCENSVELEIAF 360
 DB 301 AAKGKTEIPRHILQREFSGLSHLSKFTWCYGVRSVLYDLASVDSCENSVELEIAF 360

QY 361 HCKSPHRRMVLEPLNKLQAKWDLIPKFFLNFLCNLIYMFIFTAVAYHQTLLKQAA 420
 DB 361 HCKSPHRRMVLEPLNKLQAKWDLIPKFFLNFLCNLIYMFIFTAVAYHQTLLKQAA 420

QY 421 PHLKAEGVNSMLTGHILILGGIYLLVQGLWYFRRHVIWISFIDSYFEILFLQALL 480
 DB 421 PHLKAEGVNSMLTGHILILGGIYLLVQGLWYFRRHVIWISFIDSYFEILFLQALL 480

QY 481 TVVSQVLCFLAIEWYLLPVSALVGLWNLVYTRGFQHTGIYSVMIQKVLRLDLRFL 540
 DB 481 TVVSQVLCFLAIEWYLLPVSALVGLWNLVYTRGFQHTGIYSVMIQKVLRLDLRFL 540

QY 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMGEQDEGNGAQYRGILEASLEL 600
 DB 541 IYLVFLFGFAVALVSLSQEAWRPEAPTGNATESVQPMGEQDEGNGAQYRGILEASLEL 600

QY 601 FKFTIGMGEIAFORQLHFRGMVLLLLAYVLLTYILLNMLIAMSNTVNSVATDSWSIW 660
 DB 601 FKFTIGMGEIAFORQLHFRGMVLLLLAYVLLTYILLNMLIAMSNTVNSVATDSWSIW 660

QY 661 KLQKAIISVLENGYVWCRKQKQAGVMTVCTKPDGSDRWCPRVEEVNWSWQETLPT 720
 DB 661 KLQKAIISVLENGYVWCRKQKQAGVMTVCTKPDGSDRWCPRVEEVNWSWQETLPT 720

QY 721 LCEDPGAGVPRILENVLASPPKDEDEGASEENYVPVQLLQSN 764
 DB 721 LCEDPGAGVPRILENVLASPPKDEDEGASEENYVPVQLLQSN 764

RESULT 13
 ABU04096
 ID ABU04096 standard; protein; 764 AA.
 AC ABU04096;
 XX
 XX 29-JAN-2003 (first entry)
 DT
 XX Human expressed protein tag (EPT) #762.
 DE

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX WO200278524-A2.
 PN
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 XX (ZYCO-) ZYCOS INC.
 PA
 XX Chiciz RM, Tomlinson AJ, Urban RG;
 PI
 XX WPI; 2003-040607/03.
 DR
 XX
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 XX Example 2; SEQ ID NO 762; 134pp; English.
 PS
 XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC lymphoma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC myeloma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 6; Length 764;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSFSSPVFRLETLGGQDGEADRGKLDGSGLPMPMESQFGEDRKFPQIRVNLNY 60
 DB 1 MTSFSSPVFRLETLGGQDGEADRGKLDGSGLPMPMESQFGEDRKFPQIRVNLNY 60

QY 61 RKTGASQDPNFRDRDLNFAVSRGVPEDLAGLPEYLSKTYLTDSEYESTGKTCL 120
 DB 61 RKTGASQDPNFRDRDLNFAVSRGVPEDLAGLPEYLSKTYLTDSEYESTGKTCL 120

QY 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGSALHIAIEKRSQCCKV 180
 DB 121 MKAVLNKDGVNACILPLLQIDRDSGNPQPLVNAQCTDDYYRGSALHIAIEKRSQCCKV 180

QY 181 LKAVENGANVHARACGRFFQKQGTCTFYFGBELPLSLAACTKQWDVSVYLLNPHQASLOA 240
 DB 181 LKAVENGANVHARACGRFFQKQGTCTFYFGBELPLSLAACTKQWDVSVYLLNPHQASLOA 240

Db 181 LLVENGANVHARACGRFFQKGQCTCFYFGELPLSLAACTKQWDVSVYLLENPHQPASLOA 240
Qy 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300
Db 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300
Qy 301 AAKEGKIEIFRHLQREFSGLSLKRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIAF 360
Db 301 AAKEGKIEIFRHLQREFSGLSLKRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIAF 360
Qy 361 HCKSPHRHRMVLEPLNKLQAKWDLIPKFFLNFLCNLIYMFIFTAAYHPTLKKQAA 420
Db 361 HCKSPHRHRMVLEPLNKLQAKWDLIPKFFLNFLCNLIYMFIFTAAYHPTLKKQAA 420
Qy 421 PHLKAEGVNSMLTGHILILGGIYLLVQGLWYFMRHVPFIWISFIDSYPFELFLFOALL 480
Db 421 PHLKAEGVNSMLTGHILILGGIYLLVQGLWYFMRHVPFIWISFIDSYPFELFLFOALL 480
Qy 481 TVVSQVLCFLAIEWYLLPLLSALVIGWLNLLYYTRGFQHTGIYSVMIOKVILRDILRFL 540
Db 481 TVVSQVLCFLAIEWYLLPLLSALVIGWLNLLYYTRGFQHTGIYSVMIOKVILRDILRFL 540
Qy 541 IYLVFLFGFAVALVLSQEAWRPEAPTGNATESVQPMQEGDEGNGAAYRGILEASLEL 600
Db 541 IYLVFLFGFAVALVLSQEAWRPEAPTGNATESVQPMQEGDEGNGAAYRGILEASLEL 600
Qy 601 FKFTIGMGLAFQELHFRGMVLLLLAYVLLVYILLNNMLIALMSETVNSVATDSWSIW 660
Db 601 FKFTIGMGLAFQELHFRGMVLLLLAYVLLVYILLNNMLIALMSETVNSVATDSWSIW 660
Qy 661 KLOKATSVLEMENGYWCRKQKQAGVMTVGTGPDGSPDERWCFRVEENWASWEQTLPT 720
Db 661 KLOKATSVLEMENGYWCRKQKQAGVMTVGTGPDGSPDERWCFRVEENWASWEQTLPT 720
Qy 721 LCEDPGAGVPRILENPLVLPASPKDEDEGASEENYVPVQLQSN 764
Db 721 LCEDPGAGVPRILENPLVLPASPKDEDEGASEENYVPVQLQSN 764

RESULT 14
ADI81598
ID ADI81598 standard; protein; 764 AA.
XX ADI81598;
AC ADI81598;
XX
DT 22-APR-2004 (first entry)
XX Human vanilloid receptor-like protein 1 #2.
DE Human; calcium entry modulator; CD4536; CD5842; intracellular calcium;
XX neurological disease; inflammatory disease; cancer; Alzheimer's disease;
KW Parkinson's disease; asthma; rheumatoid arthritis; liver disease;
KW hepatitis; cirrhosis; kidney disease; glomerulonephritis.
XX
OS Homo sapiens.
XX
XX US2004009537-A1.
PN
XX
XX 15-JAN-2004.
PD
XX
XX 13-JAN-2003; 2003US-00342844.
PF
XX
XX 11-JAN-2002; 2002US-0347459P.
PR 02-AUG-2002; 2002US-0401171P.
PR 20-AUG-2002; 2002US-0405678P.
XX
XX (ROOS/) ROOS J.
PA (STAU/) STAUDERMAN K.
PA (VELI/) VELICELEBI G.
XX
PI Roos J, Stauderman K, Velicelebi G;
XX
XX WPI; 2004-090465/09.
DR

DR N-PSDB; ADI81597.
XX
PT Identifying an agent that modulates intracellular calcium levels, useful
PT for treating diseases associated with calcium dysregulation (e.g.
PT cancer), comprises monitoring the effects of the agent on store-operated
PT calcium entry.
XX
PS Disclosure; SEQ ID NO 68; 55pp; English.
XX
CC The invention relates to identifying an agent that modulates
CC intracellular calcium comprises monitoring the effects of the agent on
CC store-operated calcium entry comprising contacting one or more test cells
CC or their portion comprising one or more proteins that is (are) at least
CC about 35% homologous to the protein encoded by Drosophila gene CG4536 or
CC CG5842 over at least about 40% of the encoded protein (and that provides for
CC store-operated calcium entry with a test agent), where the portion of
CC the cell comprises the proteins, monitoring the effect(s) of the test
CC compound on store-operated calcium entry and identifying a test agent as
CC an agent if it has an effect on store-operated calcium entry. Also
CC included are a method of modulating store-operated calcium entry
CC (comprising modulating the level of, expression of, activity of or
CC molecular interactions of a protein in a cell that has altered store-
CC operated calcium entry, where the protein is at least about 35%
CC homologous to the protein encoded by Drosophila gene CG4536 or CG5842
CC over at least about 40% of the encoded protein and that provides for
CC store-operated calcium entry, and where store-operated calcium transport
CC into the cell is modulated) and a method of identifying a molecule that
CC provides for store-operated calcium entry (comprising identifying a
CC molecule that interacts with the protein mentioned above, thus,
CC identifying molecules involved in modulating store-operated calcium
CC entry. The protein does not contain the contiguous sequences appearing as
CC ADI81644 and ADI81645. The proteins are selected from ion transport
CC proteins. The method is useful in modulating, or in identifying agents
CC that modulate, intracellular calcium. These may be used in treating
CC diseases associated with calcium dysregulation, such as neurodegenerative
CC diseases (e.g. Alzheimer's disease or Parkinson's disease), inflammatory
CC diseases (e.g. asthma or rheumatoid arthritis), cancer, liver diseases
CC (e.g. hepatitis or cirrhosis) or kidney diseases (e.g.
CC glomerulonephritis). The present sequence represents an identified
CC homologue of one of the two above mentioned drosophila proteins.
XX
SQ Sequence 764 AA;
Query Match 100.0%; Score 4004; DB 8; Length 764;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTPSSSPVFRLETLDGGQDSEADRGKLDGSGLPMPMESQFGEDRKFAPIRVNLNY 60
Db 1 MTPSSSPVFRLETLDGGQDSEADRGKLDGSGLPMPMESQFGEDRKFAPIRVNLNY 60
Qy 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSTYTGSGTKTCL 120
Db 61 RKGTCASQDPNRFDRDLFNAVSRGVPEDLAGLPEYLSKTYLTDSTYTGSGTKTCL 120
Qy 121 MKAVLNKDGVNACILPILQIDRDSGNPQPLVNAOCTDDYVGHSAHIAIKRSLOQVK 180
Db 121 MKAVLNKDGVNACILPILQIDRDSGNPQPLVNAOCTDDYVGHSAHIAIKRSLOQVK 180
Qy 181 LLVENGANVHARACGRFFQKGQCTCFYFGELPLSLAACTKQWDVSVYLLENPHQPASLOA 240
Db 181 LLVENGANVHARACGRFFQKGQCTCFYFGELPLSLAACTKQWDVSVYLLENPHQPASLOA 240
Qy 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300
Db 241 TDSQGNVTLHALVMI SDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKL 300
Qy 301 AAKEGKIEIFRHLQREFSGLSLKRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIAF 360
Db 301 AAKEGKIEIFRHLQREFSGLSLKRKFTWCYGPVRVSLYDLASVDSCEENSVLEIIAF 360
Qy 361 HCKSPHRHRMVLEPLNKLQAKWDLIPKFFLNFLCNLIYMFIFTAAYHPTLKKQAA 420

361 HCKSPHRRMVVLEPLNKLQAKWDLIPKFFLNLCLNLYMFIFTAVAYHQPTLKQAA 420
421 PHLKAEGVNSMLTGHILILGGIYLLVQWLYFWRHVFVWISPTDSYFEILFLFOALL 480
421 PHLKAEGVNSMLTGHILILGGIYLLVQWLYFWRHVFVWISFIDSIFEILFLFOALL 480
481 TVVSQVLCFLAIEWYLLVLSALVGLWNLVLYYTRGFQHTGIYSVMIQVILRDLRFL 540
481 TVVSQVLCFLAIEWYLLVLSALVGLWNLVLYYTRGFQHTGIYSVMIQVILRDLRFL 540
541 IYLVFLFGFAVALVLSQEAWRPEAPTGNATESVQPMGEQDEGNGAQRGILEASLEL 600
541 IYLVFLFGFAVALVLSQEAWRPEAPTGNATESVQPMGEQDEGNGAQRGILEASLEL 600
601 FKFTIGMGLAFOELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
601 FKFTIGMGLAFOELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
661 KLOKALSVLEMENGYWCRKQKQAGVMLTVGTPDGSPPDERWCFRVEEVNWSWEQTLPT 720
661 KLOKALSVLEMENGYWCRKQKQAGVMLTVGTPDGSPPDERWCFRVEEVNWSWEQTLPT 720
721 LCEDPSGAGVPRTLENPVLASPPKEDDGDGASEENYVPVQLQSN 764
721 LCEDPSGAGVPRTLENPVLASPPKEDDGDGASEENYVPVQLQSN 764

RESULT 15

ID ADP66663
ADP66663 standard; protein; 764 AA.

AC ADP66663;

XX 26-AUG-2004 (first entry)

XX Human vanilloid 2 receptor (VR2) polypeptide, SEQ ID 2.

XX VR2; vanilloid 2 receptor; tranquilizer; antidepressant; hypnotic; CNS;
XX tocolytic; vasotropic; hypertensive; cardiovascular; gynaecological;
XX analgesic; neuroleptic; anticoagulant; gene therapy; human; receptor.

XX Homo sapiens.

XX W02004045638-A1.

XX 03-JUN-2004.

XX 18-NOV-2003; 2003WO-GB004988.

XX 18-NOV-2002; 2002GB-00026850.

XX 18-NOV-2002; 2002GB-00026865.

XX 01-OCT-2003; 2003GB-00022990.

XX (MERI) MERCK SHARP & DOHME LTD.

XX Oliver KR, Seabrook GR, Wainwright A;

XX WPI; 2004-431843/40.

XX N-PSDB; ADP66662.

XX Use of vanilloid receptor-2 ligands for treating and/or preventing
XX anxiety, depression, circadian rhythm disorders, pre-term labor, erectile
XX dysfunction, hypertension, eclampsia and/or schizophrenia.

XX Claim 20; Fig 1; 46pp; English.

XX The invention relates to a compound selected from a vanilloid 2 receptor
XX (VR2) polypeptide, a compound which modulates the activity of a VR2
XX polypeptide, a polynucleotide encoding a VR2 polypeptide, or an antisense
XX polynucleotide. The compound is used for the manufacture of a medicament
XX for treating anxiety, depression, circadian rhythm disorders, pre-term
XX labour, erectile dysfunction, hypertension and/or eclampsia and
XX associated disorders, and/or schizophrenia. The compound may also be used

CC for inducing diuresis and/or inhibiting platelet agglutination. The
CC compound may also be used for manufacturing a medicament for treating the
CC disorders mentioned above. The medicament enhances or improves sleep
CC quality and/or is used for preventing and/or treating sleep disorders and
CC sleep disturbances by increasing sleep efficiency and augmenting sleep
CC maintenance in a mammal, or for achieving a circadian rhythm phase-
CC shifting effect, for resetting the internal circadian clock or for
CC shortening the time of reentrainment of circadian rhythms in a mammal.
XX The present sequence represents a human VR2 polypeptide.

SQ Sequence 764 AA;

Query Match 100.0%; Score 4004; DB 8; Length 764;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPSSSPVFRLETLDDGGQDGEADRGKLDGSGLPMMESQFQGEDRKFAPIRVNLNY 60
DB 1 MTPSSSPVFRLETLDDGGQDGEADRGKLDGSGLPMMESQFQGEDRKFAPIRVNLNY 60
QY 61 RKGTCASQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
DB 61 RKGTCASQDPNRPDRDLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTGSTGKTCL 120
QY 121 MKAVLNLDKGVNACILPLLIQIDRDSGNPQPLVNAQCTDDYRGHSAHIAIEKRSIQCVK 180
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QY 181 LLVENGANVHARACGRFFQKGGCTCFYFGEPLSLAACTKQMDVSVLYLENPHQASLOA 240
DB 181 LLVENGANVHARACGRFFQKGGCTCFYFGEPLSLAACTKQMDVSVLYLENPHQASLOA 240
QY 241 TDSQGNVTLHALVMSIDNSAENIALVTSYDGLQAGARLCPTVQLEDIRNLQDLTFLKL 300
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QY 301 AAKEGKIEIFRHLQREFSGLSHLKFTWCYGPVRVSLYDLASVDSCEENSVLLEIAF 360
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QY 361 HCKSPHRRMVVLEPLNKLQAKWDLIPKFFLNLCLNLYMFIFTAVAYHQPTLKQAA 420
DB 361 HCKSPHRRMVVLEPLNKLQAKWDLIPKFFLNLCLNLYMFIFTAVAYHQPTLKQAA 420
QY 421 PHLKAEGVNSMLTGHILILGGIYLLVQWLYFWRHVFVWISFIDSIFEILFLFOALL 480
DB 421 PHLKAEGVNSMLTGHILILGGIYLLVQWLYFWRHVFVWISFIDSIFEILFLFOALL 480
QY 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLVLYYTRGFQHTGIYSVMIQVILRDLRFL 540
DB 481 TVVSQVLCFLAIEWYLLVLSALVGLWNLVLYYTRGFQHTGIYSVMIQVILRDLRFL 540
QY 541 IYLVFLFGFAVALVLSQEAWRPEAPTGNATESVQPMGEQDEGNGAQRGILEASLEL 600
DB 541 IYLVFLFGFAVALVLSQEAWRPEAPTGNATESVQPMGEQDEGNGAQRGILEASLEL 600
QY 601 FKFTIGMGLAFOELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
DB 601 FKFTIGMGLAFOELHFRGMVLLLLAYVLLTYILLNMLIALMSETVNSVATDSWSIW 660
QY 661 KLOKALSVLEMENGYWCRKQKQAGVMLTVGTPDGSPPDERWCFRVEEVNWSWEQTLPT 720
DB 661 KLOKALSVLEMENGYWCRKQKQAGVMLTVGTPDGSPPDERWCFRVEEVNWSWEQTLPT 720
QY 721 LCEDPSGAGVPRTLENPVLASPPKEDDGDGASEENYVPVQLQSN 764
DB 721 LCEDPSGAGVPRTLENPVLASPPKEDDGDGASEENYVPVQLQSN 764

Search completed: October 5, 2005, 11:23:48

Job time : 169 secs

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 17:21:10 ; Search time 431 Seconds
(without alignments)
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Perfect score: 2469
Sequence: 1 cagagcgagcgagcgagct.....gctggctcgtgggtccagct 2469

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2424.6	98.2	2805	3	US-09-132-316-1 Sequence 1, Appli
2	2378.4	96.3	2380	4	US-09-235-451-35 Sequence 35, Appl
3	2378.4	96.3	2380	4	US-09-235-451-35 Sequence 35, Appl
4	2259.2	91.5	2779	3	US-09-149-476-191 Sequence 151, App
5	2061.8	83.5	2860	3	US-09-149-476-314 Sequence 314, App
6	1720	69.7	1790	3	US-09-484-970B-67 Sequence 67, Appl
7	1522.4	61.7	2736	3	US-09-235-451-3 Sequence 3, Appli
8	1522.4	61.7	2736	4	US-09-235-451-22 Sequence 22, Appl
9	750.8	30.4	884	4	US-09-978-303-22 Sequence 22, Appl
10	750.8	30.4	884	4	US-09-978-303-22 Sequence 22, Appl
11	711	28.8	876	3	US-09-149-476-315 Sequence 315, App
12	662.4	26.8	4182	4	US-09-667-422-2 Sequence 2, Appli
13	662.4	26.8	4203	4	US-09-667-422-1 Sequence 1, Appli
14	660.8	26.8	2544	4	US-09-235-451-33 Sequence 33, Appl
15	660.8	26.8	2544	4	US-09-235-451-33 Sequence 33, Appl
16	660.8	26.8	3500	3	US-09-197-636-7 Sequence 7, Appli
17	660.8	26.8	4803	3	US-09-197-636-1 Sequence 3, Appli
18	660	26.7	4803	3	US-09-197-636-3 Sequence 3, Appli
19	659.2	26.7	3263	4	US-09-949-016-1066 Sequence 1066, Ap
20	659.2	26.7	3463	3	US-09-533-220A-1 Sequence 1, Appli
21	651.8	26.4	2633	4	US-09-667-422-8 Sequence 8, Appli
22	651.8	26.4	2880	4	US-09-235-451-1 Sequence 1, Appli
23	651.8	26.4	2880	4	US-09-235-451-1 Sequence 1, Appli
24	650	26.3	4171	4	US-09-667-422-3 Sequence 3, Appli
25	597.6	24.2	764	3	US-09-235-451-21 Sequence 21, Appl
26	597.6	24.2	764	4	US-09-978-303-21 Sequence 21, Appl
27	578	23.4	768	3	US-09-235-451-6 Sequence 6, Appli

28	578	23.4	768	4	US-09-978-303-6 Sequence 6, Appli
29	562.2	22.8	2616	3	US-09-500-123-5 Sequence 5, Appli
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31	535.4	21.7	2845	4	US-09-235-451-24 Sequence 24, Appl
32	535.4	21.7	2845	4	US-09-235-451-24 Sequence 24, Appl
33	506.6	20.5	2229	3	US-09-500-123-10 Sequence 10, Appl
34	506.6	20.5	4059	3	US-09-500-123-11 Sequence 11, Appl
35	501.4	20.3	650	3	US-09-235-451-7 Sequence 7, Appli
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37	465.2	18.8	3061	4	US-09-949-016-4055 Sequence 4055, Ap
38	454	18.4	454	3	US-09-132-316-19 Sequence 19, Appl
39	447	18.1	461	3	US-09-132-316-20 Sequence 20, Appl
40	415.8	16.8	430	3	US-09-132-316-23 Sequence 23, Appl
41	414	16.8	433	3	US-09-132-316-22 Sequence 22, Appl
42	405.8	16.4	431	3	US-09-132-316-67 Sequence 67, Appl
43	397.4	16.1	422	3	US-09-132-316-25 Sequence 25, Appl
44	392.8	15.9	408	3	US-09-132-316-24 Sequence 24, Appl
45	383	15.5	383	3	US-09-132-316-28 Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-132-316-1
; Sequence 1, Application US/09132316B
; Patent No. 644440
; GENERAL INFORMATION:
; APPLICANT: Young, Paul E.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Vanilloid Receptor-2
; FILE REFERENCE: 1488.1110000
; CURRENT APPLICATION NUMBER: US/09/132,316B
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: US 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5)..(2674)
US-09-132-316-1

Query Match	98.2%	Score	2424.6	DB	3	Length	2805
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Qy	63	TCCTGGCTGACCGAGC--AGCCTCTCTCTAGGATGACCTCACCTCCAGCTCTCCA	120				
Db	347	TCCTGGCTGACCGAGCTATGCTCTCTCTAGGATGACCTCACCTCCAGCTCTCCA	406				
Qy	121	GTTCACAGTTGGAGACATTAGATGGAGGCGCAAGAGATGGCTTGAGGGGAGGAGGAGGA	180				
Db	407	GTTCACAGTTGGAGACATTAGATGGAGGCGCAAGAGATGGCTTGAGGGGAGGAGGAGGA	466				
Qy	181	AAGCTGATTTTGGAGCGGCTGCTCCATGAGTACAGTTCACAGGCGGAGGACCGG	240				
Db	467	AAGCTGATTTTGGAGCGGCTGCTCCATGAGTACAGTTCACAGGCGGAGGACCGG	526				
Qy	241	AAATTCGCCCTCAGATAAGAGTCAACTCACTACCGAAAGGAAACAGGTGCCAGTCAG	300				
Db	527	AAATTCGCCCTCAGATAAGAGTCAACTCACTACCGAAAGGAAACAGGTGCCAGTCAG	586				

Qy	1039	CAGCGGAGTTTTTTCAGGACTGACCACTTTTCCGAAAGTTTACCGAGTGGTCTATGGG	1098
Db	961	CAGCGGAGTTTTTTCAGGACTGACCACTTTTCCGAAAGTTTACCGAGTGGTCTATGGG	1020
Qy	1099	CTGTGCGGGTGTGCTGTATGACCTTGTGAGCAGCTGTGAGGAGAACTCAGTG	1158
Db	1021	CTGTGCGGGTGTGCTGTATGACCTTGTGAGCAGCTGTGAGGAGAACTCAGTG	1080
Qy	1159	CTGGAGATCATGCTTTTCAATGCAAGAGCCCGACCGACACCGAATGGTCTTTTAAAC	1218
Db	1081	CTGGAGATCATGCTTTTCAATGCAAGAGCCCGACCGACACCGAATGGTCTTTTAAAC	1140
Qy	1219	CCCTGGAACAACTGCTGAGGGGAAATGGATCTGCTCATCCCAAGTTCTTTTAAAC	1278
Db	1141	CCCTGGAACAACTGCTGAGGGGAAATGGATCTGCTCATCCCAAGTTCTTTTAAAC	1200
Qy	1279	TTCTGTGTAATCTGATCTACATGTTTCATCTTCCACCGCTGTGCTTACCATCAGCTACC	1338
Db	1201	TTCTGTGTAATCTGATCTACATGTTTCATCTTCCACCGCTGTGCTTACCATCAGCTACC	1260
Qy	1339	CTGAAGACAGCGCGCCCTCCTGAAAGCGGAGTTGGAAATCTCATGCTGCTGACG	1398
Db	1261	CTGAAGACAGCGCGCCCTCCTGAAAGCGGAGTTGGAAATCTCATGCTGCTGACG	1320
Qy	1399	GGCCACATCTTATCTGTAGGGGATCTACTCTCTGCTGGGCCAGCTGTGCTACTTC	1458
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Qy	1459	TGGCGGCGCACGTGTTTCATCTGATCTCGTTTCATAGACAGCTACTTTGAAATCTCTTC	1518
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Qy	1519	CTGTTCCAGGCCCTGTCTACAGTGGTCCAGGTGCTGTGTTTCTGGCCATCGAGTGG	1578
Db	1441	CTGTTCCAGGCCCTGTCTACAGTGGTCCAGGTGCTGTGTTTCTGGCCATCGAGTGG	1500
Qy	1579	TACTGCGCTGTGTTGCTGCGCTGGTCTGGCTGGCTGCACTCTTTACTATACA	1638
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Qy	1639	CGTGGCTTCAGACACAGGCATCTACAGTGTATGATCCAGAGGTCTATCTCGCGGAC	1698
Db	1561	CGTGGCTTCAGACACAGGCATCTACAGTGTATGATCCAGAGGTCTATCTCGCGGAC	1620
Qy	1699	CTGCTGCGCTTCTTGTGATCTACTAGTCTTCTTTTCGGCTTGGCTAGCCCTGGTG	1758
Db	1621	CTGCTGCGCTTCTTGTGATCTACTAGTCTTCTTTTCGGCTTGGCTAGCCCTGGTG	1680
Qy	1759	AGCTGAGCCAGGAGGCTTGGCGCCCGAAGCTCTACAGGCCCAATGCCAGAGTCA	1818
Db	1681	AGCTGAGCCAGGAGGCTTGGCGCCCGAAGCTCTACAGGCCCAATGCCAGAGTCA	1740
Qy	1819	GTGAGCCCATGGAGGACAGGAGACGAGGGCAACCGGGCCCACTAGTACAGGGTATCCTG	1878
Db	1741	GTGAGCCCATGGAGGACAGGAGACGAGGGCAACCGGGCCCACTAGTACAGGGTATCCTG	1800
Qy	1879	GAAGCCTCTTGGAGCTTCTCAAAATTCACCATCGGCATGGCGAGCTGGCTTCCAGGAG	1938
Db	1801	GAAGCCTCTTGGAGCTTCTCAAAATTCACCATCGGCATGGCGAGCTGGCTTCCAGGAG	1860
Qy	1939	CAGCTGCATCTCCGCGGATGGTGTGCTGTGCTGCTGCGCTACGTGCTCACCTAC	1998
Db	1861	CAGCTGCATCTCCGCGGATGGTGTGCTGTGCTGCTGCGCTACGTGCTCACCTAC	1920
Qy	1999	ATCTGCTGTCTCAACATGCTCATCGCCTCATAGAGCAGACCGTCAACAGTGTGCCACT	2058
Db	1921	ATCTGCTGTCTCAACATGCTCATCGCCTCATAGAGCAGACCGTCAACAGTGTGCCACT	1980
Qy	2059	GACAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCTGGAGTGAAGTGGC	2118
Db	1981	GACAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCTGGAGTGAAGTGGC	2040
Qy	2119	TATTTGGTGGTGCAGGAAGACAGCGGGCAGGTGTGATGCTGACCGTTGGCACTAAGCCA	2178
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Qy	2179	GATGGAGCCCGGATGAGCGCTGTGCTTTCAGGTTGAGGAGGTGAACCTGGCTTCATGG	2238
Db	2101	GATGGAGCCCGGATGAGCGCTGTGCTTTCAGGTTGAGGAGGTGAACCTGGCTTCATGG	2160
Qy	2239	GAGCAGACGCTCCCTACGCTGTGTAGGACCCCTCAGGGGACAGGTGTCCCTCGAACTCTC	2298
Db	2161	GAGCAGACGCTCCCTACGCTGTGTAGGACCCCTCAGGGGACAGGTGTCCCTCGAACTCTC	2220
Qy	2299	GAGAACCCCTGTCTGCTTCCCTCCCAAGGAGGATGAGATGGTGGCTCTGAGGAAAAC	2358
Db	2221	GAGAACCCCTGTCTGCTTCCCTCCCAAGGAGGATGAGATGGTGGCTCTGAGGAAAAC	2280
Qy	2359	TATTTGGCCGCTCAGCTCTCCAGTCCCAACTGATGCGCCAGATGCGAGGAGGCCAGAG	2418
Db	2281	TATTTGGCCGCTCAGCTCTCCAGTCCCAACTGATGCGCCAGATGCGAGGAGGCCAGAG	2340
Qy	2419	GACAGAGCAGAGATCTTTCCAAACCAACATCTGCTGGCTCT	2458
Db	2341	GACAGAGCAGAGATCTTTCCAAACCAACATCTGCTGGCTCT	2380

RESULT 4

US-09-149-476-191
; Sequence 191, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
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; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23

[illegible]

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 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/057,669
 EARLIER FILING DATE: 1997-09-05
 EARLIER APPLICATION NUMBER: 60/049,610
 EARLIER FILING DATE: 1997-06-13
 EARLIER APPLICATION NUMBER: 60/061,060
 EARLIER FILING DATE: 1997-10-02

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Best Local Similarity 96.5%; Pred. No. 0;
 Matches 2365; Conservative 10; Mismatches 5; Indels 70; Gaps 4;

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 1460 GCGCGGCCACAGTGTTCATCTGATCTGCTTATAGACAGCTACTTTTGAATCTCTTCTTC 1519
 1757 GCGCGGCCACAGTGTTCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1816
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 1640 GTGCTTTCAGCACACAGGCTCTACAGTGTCTATGATCCAGAGGTCATCTCTGCGGAGC 1699
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; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09149,476
; CURRENT FILING DATE: 1998-09-08
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; EARLIER APPLICATION NUMBER: 60/049,610
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; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Best Local Similarity 95.1%; Pred. No. 0;
Matches 2364; Conservative 4; Mismatches 31; Indels 86; Gaps 20;

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US-09-235-451-3
; Sequence 3, Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: R. rattus
; FEATURE:
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QY	88	CTCTCTAGGATGACCTCACCTCCAGCTCTCCAGTTTTTCAGGTTGGAGACATTTAGATGA	147			
DB	322	-CTCTCAGGATGACTTCAGCTCCAGCCCTCCAGCTTCAGGCTGGAGACTTCGGATGA	380			
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DB	381	GATGAAGAGGCAATGTCTGAGGTGAACAAGGGGAAGCAGGA-----ACCGCCC	428			
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DB	969	CTTCTCTGCTGGTGCAACAGCAGTGGGATGTGTGACCTTACCTCTCTCTGGAGAACCCA	1028			
QY	793	CACAGCCCGCCAGCTCGAGGCCACTGACTCCAGGGGCAACAGTCTCTGCAATGCCCTA	852			
DB	1029	CACAGCCCGCCAGCTGGAGGCCACCGACTCTCCTGGGCAACAGTCTCTGCTGCTCTG	1088			
QY	853	GTGATGATCTCGGACAACTCAGCTGAGAAACATTTGCACTGTGTGACCAAGCATGTATGAG	912			
DB	1089	GTAAATGATTGAGATAACTCGCCCTGAGAAACAGTGTGCTGCTGATTCACATGTACGACGG	1148			
QY	913	CTCTCTCAAGCTGGGGCGCCCTCTGCCCTACCGTGCAGCTTCAGGACATCCGCAACCTG	972			
DB	1149	CTTCTCAAAATGGGGCGCCCTCTGCCCCACTGTGTGACAGCTTGAAGGAAATCTCCAACC	1208			
QY	973	CAGGATCTCAGGCTCTGAAGCTGGCGCCCAAGAGGGCAAGATCGAGATTTTCAGGCAC	1032			
DB	1209	CAAGGCTCACACCCCTGAAACTAGCGGCCCAAGGAGGCAAAATCGAGATTTTCAGGCAC	1268			
QY	1033	ATCTCTGACGGGAGTTTTTCAGGACTGAGCCA---CCTTTCCGAAAGTTCCACGAGTGG	1089			
DB	1269	ATCTCTGACGGGAAATTTTCAGGACCGTACAGCCCTTTCCGAAAGTTTACTGAGTGG	1328			
QY	1090	TGCTATGGCCCTGTCCGGGTGCTGTATGACCTCGGCTTCTGTGACAGCTGTGTGAGGAG	1149			
DB	1329	TGTTACGGTCTGTGGGGTATCGCTGTACGACCTGTCTCTGTGGACAGCTGGGAAAG	1388			
QY	1150	AACTCAGTGTCTGAGANCAATGCTTTTCAATGCAAGAGCCCGCAACCGAACCGAATGGTC	1209			
DB	1389	AACTCGGTCTGAGATCATCGCTTTTCAATGCAAGAGCCCGAAACCGGACCGCATGTGTG	1448			
QY	1210	GTTTTGGAGCCCTGCAACAACTGTGTGAGGGGAAATGGGATCTGTCTATCCCAAGTTC	1269			
DB	1449	GTTTTAGAACCACTGAACAAGCTTCTGCAGGAGAAATGGGATCGGCTCTCTCAAGATTC	1508			
QY	1270	TTCTTAAACTCTCTGTGTAATCTGATCTACATGTTCATCTTTCACCGCTCTTGGCTACCAT	1329			
DB	1509	TTCTTCAACTTCGCTGTCTACTTGGTCTACATGTTCATCTTTCACCGCTCTTGGCTACCAT	1568			
QY	1330	CAGCTTACCTGAAAGAGCAGCGCCCTCTCACTGAAAGCGGAGGTTGGAAACTCCATG	1389			
DB	1569	CAGCTTCTCCCTGATCAGCCAGCCATCCCTCATCAAAAGCGACTTTTGGGGAATCCATG	1628			
QY	1390	CTGCTGACGGGCCACATCTTATCTGTAGGGGGATCTACTCTCTGCTGGGCCAGCTG	1449			
DB	1629	CTGCTGCTGGGCCACATCTGATCTCTGTGGGGGTATTTACTCTTACTTGGGCCAGCTG	1688			
QY	1450	TGCTACTTCTGGCGGCCACCGTGTTCATCTCGATCTCTGTTTCATAGACAGCTACTTTGAA	1509			
DB	1689	TGCTACTTTTGGCGGGCGCTGTTTATCTGATCTCATTCATGACAGCTACTTTTGA	1748			
QY	1510	ATCTCTTCTCTGTTCCAGGCCCTCTCAAGTGGTGTCCAGGTGTCTGTTCCTGGCC	1569			
DB	1749	ATCTCTTCTCTGTTCCAGGCTCTGTCTCAAGTGTGTCTCCAGGTGTCTGTTCATGAG	1808			
QY	1570	ATCGAGTGTACTCGCCCTGTGTGTCTGCGCTGTGTCTGGCTGTGGCTGGAACCTGCTT	1629			
DB	1809	ACTGAATGTACTCTACCCCTGTGTGTATCCCTAGTGTCTGGCTGTGGCTGTGAACTGCTT	1868			
QY	1630	TACTATACAGTGGCTTCCAGCACACAGGCATCTACAGTGTCTATGATCCAGAGGTCACT	1689			
DB	1869	TACTACACAGGGCTTTTCAGCACACAGGCATCTACAGTGTCTATGATCCAGAGGTCACT	1928			
QY	1690	CTGGGGAGCTGTGGCTTCTCTGTGATCTATTAGTCTTCTCTTTCGGCTGTGCTGTA	1749			
DB	1929	CTTCGAGACTGCTCGGTTTCTGTGTGTCTACCTGTGTCTCTTTCGGCTTGTGCTGTA	1988			
QY	1750	GCCTGTGAGCTGTGAGCAGGAGGCTTGGCGCCCGAAGCTCTACAGGCCCAATGCC	1809			
DB	1989	GCCTGTAGTAAAGCTTGAAGAGAGGCGCCGAAGTCCCAAGCCCTCTGAAGATCAACTCC	2048			
QY	1810	ACAGAGTCAAGTTCAGCCCATGGAGGACAGAGGAGCAGGGCAACCGGGGCCCATGACAG	1869			
DB	2049	ACAGTGAAGGACACCCACGCTGGGCCAGAGGAGGAGGCC-----AGCTCATATCGG	2102			
QY	1870	GTATCTCTGGAAGCTCTCTTGGAGCTCTTCAAAATTCACCATCGGCAATGGGGAGCTGGCC	1929			
DB	2103	AGCATCTGGAATGCTCTCTCTAGAGCTGTTCAAGATTCACCATTTGGTATGGGGAGCTGGCT	2162			
QY	1930	TTCCAGGAGCAGCTGACATTCGCGCATGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT	1989			
DB	2163	TTCCAGGAAACAGCTGGGTTTTCTGGGGTGGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT	2222			
QY	1990	CTCACCTCATCTCTGTCTCAACATGTCTCATCGCCCTCATGAGCGAGACCGTCAACAGT	2049			
DB	2223	CTCACCTAGCTCTGCTGTCAACATGTCTCATTTGCTCTCATGAGCGAAACTGTCAACAC	2282			
QY	2050	GTGCGCATGACAGCTGGAGCATCTGGAAGCTGCAAGAACCCATCTCTCTCTCTGGAGATG	2109			
DB	2283	GTGTCTGCAACAGCTGGAGCATCTGGAAGTGTGCAAGAACCCATCTCTCTCTCTGGAGATG	2342			
QY	2110	GAGAATGGCTATTGTTGGTGTGC---AGGAAGAGCAGCGGGCAGGTGTGTGTGTGTGTGT	2166			

Db	471	GTCTTGAGATGGAGAAATGGCTATTGTGTGTGACGAAGAAGCAGCGGGCAGGTGTGATG	530
Qy	2158	CTGACCTTTGGCACTAAGACCAGATGGCAGCCCGGATGAGCGCTTGGTCTTTCAGGGTGGAG	2217
Db	531	CTGACCTTTGGCACTAAGACCAGATGGCAGCCCGGATGAGCGCTTGGTCTTTCAGGTGGAG	590
Qy	2218	GAGGTGAATCGGGCTTCATGGGACAGACGCTGCCTACGCTGTGTGAGGACCCGTCAGGG	2277
Db	591	GAGGTGAATCGGGCTTCATGGGACAGACGCTGCCTACGCTGTGTGAGGACCCGTCAGGG	650
Qy	2278	GCAGGTGTCCTTCGAACTCTCGAGAACCTGTCTCTGGCTTTCCCTCCACGAGGAGGATGAG	2337
Db	651	GCAGGTGTCCTTCGAACTCTCGAGAACCTGTCTCTGGCTTTCCCTCCACGAGGAGGATGAG	710
Qy	2338	GATGGTGCCTCTGAGGAAAACTATGTGCCCGTCCAGCTCTCTCCAGTCCAACTGATGGCCC	2397
Db	711	GATGGTGCCTCTGAGGAAAACTATGTGCCCGTCCAGCTCTCTCCAGTCCAACTGATGGCCC	770
Qy	2398	AGATGCACGAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCCAACCACTCTGCTGGCTC	2457
Db	771	AGATGCACGAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCCAACCACTCTGCTGGCTC	830
Qy	2458	TGGGGTCCCAGT	2469
Db	831	TGGGGTCCCAGT	842

RESULT 10

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1  RESULT 10
2  US-09-978-303-22
3  ; Sequence 22, Application US/09978303
4  ; Patent No. 6790629
5  ; GENERAL INVENTION:
6  ; APPLICANT: Julius, David J.
7  ; APPLICANT: Caterina, Michael J.
8  ; APPLICANT: Brake, Anthony J.
9  ; TITLE OF INVENTION: Nucleic acid sequences encoding
10 ; TITLE OF INVENTION: capsaicin receptor and capsaicin receptor-related
11 ; TITLE OF INVENTION: polypeptides and uses thereof
12 ; FILE REFERENCE: UCAL084CON
13 ; CURRENT APPLICATION NUMBER: US/09/978,303
14 ; CURRENT FILING DATE: 2001-10-15
15 ; PRIOR APPLICATION NUMBER: 09/235,451
16 ; PRIOR FILING DATE: 1999-01-22
17 ; PRIOR APPLICATION NUMBER: 60/072,151
18 ; PRIOR FILING DATE: 1998-01-22
19 ; PRIOR APPLICATION NUMBER: 08/915,461
20 ; PRIOR FILING DATE: 1997-08-20
21 ; NUMBER OF SEQ ID NOS: 48
22 ; SOFTWARE: FastSeq for Windows Version 4.0
23 ; SEQ ID NO 22
24 ; LENGTH: 884
25 ; TYPE: DNA
26 ; ORGANISM: Homo sapiens
27  US-09-978-303-22

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	Query Match	30.4%;	Score 750.8;	DB 4;	Length 884;
	Best Local Similarity	92.0%;	Pred. No. 4.9e-180;		
	Matches 839;	Conservative	3;	Mismatches 0;	Indels 70; Gaps 2;
Qy	1558	TGTTTCTCGGCCATCGAGTGGTACTCTGCCCTGCTGTGTCTGCGTGTGCTGGGCTGG	1617		
Db	1	TGTTTCTCGGCCATCGAGTGGTACTCTGCCCTGCTGTGTCTGCGTGTGCTGGGCTGG	60		
Qy	1618	CTGAACCTGTTTACTATATACACGTGGCTTCCAGCACACAGGCATCTACAGTGCATGATC	1677		
Db	61	CTGAACCTGTTTACTATATACAGTGGCTTCCAGCACACAGGCATCTACAGTGCATGATC	120		
Qy	1678	CAGAAGTGCATCTGTCGGGACCTGCTGGCTTCTTCTGATCTACTTAGTCTCCTTTTC	1737		
Db	121	CAGA-----CAGA-----	124		
Qy	1738	GGCTTCGCTGTAGCCCTGGTGAGCCTGAGCCAGGAGCCTTGGGCCCCCGAAGCTCCTACA	1797		

RESULT 11
US-09-149-476-315
; Sequence 315, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07

125	Db	-----AGCCCTGGTGAGCCTGAGCCAGGA---TTGGCGCCCGGAAGCTCCTTACA	170
1798	Qy	GGCCCCAATGCCACACAGAGTCAGTGCAGCCCATCGAGGGACAGAGAGCAGAGGGCAACGGG	1857
171	Db	GGCCCCAATGCCACACAGAGTCAGTGCAGCCCATCGAGGGACAGAGAGCAGAGGGCAACGGG	230
1858	Qy	GCCCACTACAGGGGTATCTGGAAAGCCTCTTTGGAGCTCTTCAAAATTCACCATCGGCATG	1917
231	Db	GCCCACTACAGGGGTATCTGGWAGGCTCTTTGGAGCTCTTCAAAATTCACCATCGGCATG	290
1918	Qy	GGCGAGCTGCGCTTTCAGAGAGCAGCTGCATCTCCGGGGCATGGTGTGCTGCTGCTGCTG	1977
291	Db	GGCGAGCTGCGCTTTCAGAGAGCAGCTGCATCTCCGGGGCATGGTGTGCTGCTGCTGCTG	350
1978	Qy	GCCTACGTGCTGCTCACCTACATCTCTGCTCTCAACATGCTCATCGCCCTCATGAGCGAG	2037
351	Db	GCCTACGTGCTGCTCACCTACATCTCTGCTCTCAACATGCTCATCGCCCTCATGAGCGAG	410
2038	Qy	ACCGTCAACAGTGTGCGCACTGACAGCTTGAGCATCTGGAAGCTGCGAAGAAGCCATCTCT	2097
411	Db	ACCGTCAACAGTGTGCGCACTGACAGCTTGAGCATCTGGAAGCTGCGAAGAAGCCATCTCT	470
2098	Qy	GTCTCGAGATGAGAAATGGCTATTGGTGTGCGAGGAAGACAGCGGGCAGGTTGTGATG	2157
471	Db	GTCTCGAGATGAGAAATGGCTATTGGTGTGCGAGGAAGACAGCGGGCAGGTTGTGATG	530
2158	Qy	CTGACCGTTGGCACTAAGCCAGATGGCAGCGCCGGATGAGCGCTGGTGCCTTCAGGGTGGAG	2217
531	Db	CTGACCGTTGGCACTAAGCCAGATGGCAGCGCCGGATGAGCGCTGGTGCCTTCAGGGTGGAG	590
2218	Qy	GAGGTGAATGGGCTTCATGGGAGCAGACGCTGCCTACGTTGTTGAGGACCCGTCAGGG	2277
591	Db	GAGGTGAATGGGCTTCATGGGAGCAGACGCTGCCTACGTTGTTGAGGACCCGTCAGGG	650
2278	Qy	GCAGGTGTCCCTCGAATCTCGAAGACCTGTCTCGCTTCCCCTCCAGAGGAGATGAG	2337
651	Db	GCAGGTGTCCCTCGAATCTCGAAGACCTGTCTCGCTTCCCCTCCAGAGGAGATGAG	710
2338	Qy	GATGGTGCCTCTCAGGAAAATATGTGCCCGTCCAGCTCCTCCAGTCCAACTGATGGGCC	2399
711	Db	GATGGTGCCTCTCAGGAAAATATATGTGCCCGTCCAGCTCCTCCAGTCCAACTGATGGGCC	770
2398	Qy	AGATGCAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCCAAACCACTGCTGGCTC	2457
771	Db	AGATGCAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCCAAACCACTGCTGGCTC	830
2458	Qy	TGGGGTCCCAGT 2469	
831	Db	TGGGGTCCCAGT 842	

1	EARLIER FILING DATE: 1997-06-06	
2	EARLIER APPLICATION NUMBER: 60/056,886	
3	EARLIER FILING DATE: 1997-08-22	
4	EARLIER APPLICATION NUMBER: 60/056,877	
5	EARLIER FILING DATE: 1997-08-22	
6	EARLIER APPLICATION NUMBER: 60/056,889	
7	EARLIER FILING DATE: 1997-08-22	
8	EARLIER APPLICATION NUMBER: 60/056,893	
9	EARLIER FILING DATE: 1997-08-22	
10	EARLIER APPLICATION NUMBER: 60/056,630	
11	EARLIER FILING DATE: 1997-08-22	
12	EARLIER APPLICATION NUMBER: 60/056,878	
13	EARLIER FILING DATE: 1997-08-22	
14	EARLIER APPLICATION NUMBER: 60/056,662	
15	EARLIER FILING DATE: 1997-08-22	
16	EARLIER APPLICATION NUMBER: 60/056,872	
17	EARLIER FILING DATE: 1997-08-22	
18	EARLIER APPLICATION NUMBER: 60/056,882	
19	EARLIER FILING DATE: 1997-08-22	
20	EARLIER APPLICATION NUMBER: 60/056,637	
21	EARLIER FILING DATE: 1997-08-22	
22	EARLIER APPLICATION NUMBER: 60/056,903	
23	EARLIER FILING DATE: 1997-08-22	
24	EARLIER APPLICATION NUMBER: 60/056,888	
25	EARLIER FILING DATE: 1997-08-22	
26	EARLIER APPLICATION NUMBER: 60/056,879	
27	EARLIER FILING DATE: 1997-08-22	
28	EARLIER APPLICATION NUMBER: 60/056,880	
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30	EARLIER APPLICATION NUMBER: 60/056,874	
31	EARLIER FILING DATE: 1997-08-22	
32	EARLIER APPLICATION NUMBER: 60/056,910	
33	EARLIER FILING DATE: 1997-08-22	
34	EARLIER APPLICATION NUMBER: 60/056,864	
35	EARLIER FILING DATE: 1997-08-22	
36	EARLIER APPLICATION NUMBER: 60/056,636	
37	EARLIER FILING DATE: 1997-08-22	
38	EARLIER APPLICATION NUMBER: 60/056,874	
39	EARLIER FILING DATE: 1997-08-22	
40	EARLIER APPLICATION NUMBER: 60/056,910	
41	EARLIER FILING DATE: 1997-08-22	
42	EARLIER APPLICATION NUMBER: 60/056,892	
43	EARLIER FILING DATE: 1997-08-22	
44	EARLIER APPLICATION NUMBER: 60/057,761	
45	EARLIER FILING DATE: 1997-08-22	
46	EARLIER APPLICATION NUMBER: 60/047,595	
47	EARLIER FILING DATE: 1997-05-23	
48	EARLIER APPLICATION NUMBER: 60/047,599	
49	EARLIER FILING DATE: 1997-05-23	
50	EARLIER APPLICATION NUMBER: 60/047,588	
51	EARLIER FILING DATE: 1997-05-23	
52	EARLIER APPLICATION NUMBER: 60/047,585	
53	EARLIER FILING DATE: 1997-05-23	
54	EARLIER APPLICATION NUMBER: 60/047,590	
55	EARLIER FILING DATE: 1997-05-23	
56	EARLIER APPLICATION NUMBER: 60/047,594	
57	EARLIER FILING DATE: 1997-05-23	
58	EARLIER APPLICATION NUMBER: 60/047,589	
59	EARLIER FILING DATE: 1997-05-23	
60	EARLIER APPLICATION NUMBER: 60/047,593	
61	EARLIER FILING DATE: 1997-05-23	
62	EARLIER APPLICATION NUMBER: 60/047,614	
63	EARLIER FILING DATE: 1997-05-23	
64	EARLIER APPLICATION NUMBER: 60/043,578	
65	EARLIER FILING DATE: 1997-04-11	
66	EARLIER APPLICATION NUMBER: 60/043,576	
67	EARLIER FILING DATE: 1997-04-11	


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Db      730  ACCATCCCTGCTCTGGAGATCGCGGCAAAACGACAGCTGAAGGAGCTTGTCAAC 789
Qy      556  GCCAGTGCACAGATGATATTAACGAGGCCACAGCGCTCTGACATTCGCCATTTGAGAAG 615
Db      790  GCCAGCTACAGGACAGCTACTACAAGGGCCACAGACAGCACTGCACATCGCCATCGAGAGA 849
Qy      616  AGGAGTCTGAGTGTGTGAGCTCTGTTGGAGATGGGGCCAAATGTGATGCCCGGGCC 675
Db      850  CGAACATGCGCTGTGTGAGCCCTCTGTTGGAGAACGGAGCAGACGTCCAGGCTCGGGCC 909
Qy      676  TGGCGCGCTTCTTCAGAAAGGCCCAAG---GGACTTGTCTTTTAATTTCCGTTGAGCTACCC 732
Db      910  CATGGGACCTCTTTAAGAAACCAAAAGGGGCGCTGGATTTCTACTTGGTGAATGCCCC 969
Qy      733  CTCTCTTTGGCCCTTGCACCAAGCAGTGGGATGTGTGAAGCTACCTCTCTGGAGAACCCA 792
Db      970  CTGTCCCTGGCGGTGACCAACACAGCTGGGCACTCGTGAAGTTCTCTGTCTGCAGAACTCC 1029
Qy      793  CACAGCGCCGACCTGTGAGGCACTGACTCCAGGGCAACACAGTCCCTGTCATGCCCTA 852
Db      1030  TGGCAGACGCGCCGACATCAGCGCCAGGACTCGGTGGGCAACCGTGTGCAAGCCCTG 1089
Qy      853  GTGATGATCTCGACAACTCAGCTGAGAACATTTGCACTGTGTGACCAAGCATGTATGATGG 912
Db      1090  GTGAGTGTGCGACAAACACGGCCGACACACGAAATTTGTGAGGAGCATGTACAATGAG 1149
Qy      913  CTCTCTCAAGCTGGGGCCGCTCTGCTGCTACCGTGCAGCTTGAAGCATTCGCGAACCTG 972
Db      1150  ATTCTGATGTGGGGCCAAACTGCACCCGACGTGAAGCTGGAGGAGCTCACCACAAAG 1209
Qy      973  CAGGATCTCAGCTCTGAAGCTGGCGCCGACAGGAGGCAAGATCGAGATTTTCAGGCAC 1032
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Qy      1033  ATCTCTGAGCGGGAGTT-----TTCAGGACTGAGCCACCTTTCCCGAAAGTTTCAACCGAG 1086
Db      1270  ATTTCTCAGCGGAGATTCAGGAGCCCGAGTGACGAGCACTGTGCCAGAAATTTCAACGAG 1329
Qy      1087  TGTGTCTATGGGCTGTCCGGGTGTCTGTGTATGACTGTGCTTCTGTGGACAGCTGTGAG 1146
Db      1330  TGGGCTTACGGGCGGTGCACTCTGCTGTATGACGACCTGTCTGATCGACACCTCGCGAG 1389
Qy      1147  GAGAACTCAGTGTGGAGATTTGCTTTTCAATTGCA---AGAGCCCGCACCGACCGGA 1203
Db      1390  AAGAACTCGTGTGGAGGTATCGCTTACAGCAGCAGCGAGACCCCTTAATTCGCGACGAC 1449
Qy      1204  ATGCTGTCTTTGGAGCCCTGAAACAAACTGTGTGAGCGGAAATGGGA---TCTGCTCATC 1260
Db      1450  ATGCTCTTTGGAGCCGCTGAAACCGACTCTGTGAGGACAAAGTGGGACAGATTCGTCAAG 1509
Qy      1261  CCCAAGTTCTTTAAACTTCTGTGTAATCTGATCTACATGTTTCATCTTCAACGCTGTT 1320
Db      1510  CGCATCTTCTACTTCAACTTCTGTCTACTGTCTGCTGATGATGATCATCTTCAACCATGGT 1569
Qy      1321  GCCTACCATCAGCTTACCTGAAAGACAGGCGCCCTCACCCTGAAGCGGAGTTGGA 1380
Db      1570  GCCTACTACAGGCC-----CGTGGATGGCTTGGCTCCCTTTAAGATGGAAAAAATTGGA 1623
Qy      1381  AACTCCATGCTGTGAGGGCCACATCTTATCTGTCTAGGGGGATCTACTCTCTGCTG 1440
Db      1624  GACTATTTCCGAGTACTGGAGAGATCTGTCTGTGTGTAGGAGAGTACTTCTTTTTC 1683
Qy      1441  GCGCAGCTGTGTACTTCTGGCGGCCACAGTGTTCATCTGATCTCTGTTCAATAGACAGC 1500
Db      1684  CGAGGATTCAGTATTTCTTCAGAGGGCGCGTGCATGAAAGACCTGTTGTGTGACAGC 1743
Qy      1501  TACTTTGAAATCTCTTCTGTTCCAGGCCCTGTCTCAGTGTGTCTCCAGTGTCTGTGT 1560
Db      1744  TACAGTGAAGTGTCTTTCTTTCTGCAATCACTGTGTCTGCTGGCCACCGTGTGTGTAC 1803
Qy      1561  TTCTCTGGCCATCGAGTGTACTGCCCCCTGTGTGTCTGCTGTGTCTGGCTGGCTGTG 1620

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Db      1804  TTCAGCCACTCAAGGAGTATGTGGCTTCCATGGTATTCTCCTGGCCTTGGGCTGGACC 1863
Qy      1621  AACCTGCTTTTACTATACAGTGGCTTCCAGCAACAGGCACTACAGTGTCTATGATCCAG 1680
Db      1864  AACATGCTCTACTATACCCCGGTTTCCAGCAGATGGGCACTATATGCCCTCATGATAGAG 1923
Qy      1681  AAGGTCACTCTCGGGAACCTGTGGCTTCTTCTGATCTACTAGTCTTCTTTTTCGGC 1740
Db      1924  AAGATGATCTCTGAGAGACCTGTGCGTTCATGTTTGTCTACATCTCTTCTTGTTCGGG 1983
Qy      1741  TTCGCTGTAGCCCTGTGTAGCTGAGCAGGAGGCTTGGCGCCCGGAAAGCTCTCAAGGC 1800
Db      1984  TTTTCCACAGCGTGTGTGACGCTGATTGAAGACGGGAAGAACTACTCCCTGCGCTGAG 2043
Qy      1801  CCCAATGCCACAGAGTCACTGTCAGCCCATGAGGGGACAGAGGACGAGGGCAACGGGGCC 1860
Db      2044  TCCACGTC-----GCACAGGTGCGGGGCTTGCCTGACAGGCCCCCGGATAGC 2091
Qy      1861  CAGTACAGGGGTATCTCGAAGCCTCTTTGGAGCTCTTCAAATTTCAATTCGCGCATGGGC 1920
Db      2092  TCTTCAACACAGCTGTACTCCACCTGCTGGAGCTGTTCAAAGTTCAACCATCGGCATGGGC 2151
Qy      1921  GAGTGGCCCTTCAGAGCAGCTGACCTTCCGGCGGCAATGGTGTGTGCTGTGCTGTGGCC 1980
Db      2152  GACCTGGAGTTCACTGAGAACTATGACTTCAAGGCTGTCTTCATCATCTCTGCTGTGGCC 2211
Qy      1981  TAGGTGCTGCTCACCTPACATCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACC 2040
Db      2212  TATGTAATTTCTACCTTACATCTCTCTGCTCAACATGCTCATCGCCCTCATGSGTGAGACT 2271
Qy      2041  GTCAACAGTGTGCCACTGACAGCTGGAGCATCTGGAAGCTGCAAGAGCAATCTCTGTCT 2100
Db      2272  GTCAACAGATCGCACAGAGAGCAAGAACATCTGGAAGCTGCAGAGAGCCATCACCATC 2331
Qy      2101  CTGAGATGAGAAATGGCTTATGGTGTGTGAGGAGAG---CAGCGGGCAGGTGTGATG 2157
Db      2332  CTGGACACGAGGAAGAGCTTCTTAAATGTCATGAGGAAGGCTTTCGCTCAGGCAAGCTG 2391
Qy      2158  CTGACCGTTGGCACTAAGCCAGATGCGAGCCCGATGAGCGCTGAGCGCTTTCAGGGTGGAG 2217
Db      2392  CTGAGGTGGGTATACACCTGATGAGGAGAGCACTACCGGTGGTGTTCAGGGTGGAC 2451
Qy      2218  GAGTGAATCGGCTTTCATGGGAGCAGACGCTGCTACGCTGTGTGTGAGGACCCG 2271
Db      2452  GAGTGAATCGGACCACCTGGAACACCAACGTTGGGATCATCAACGAAGACCCG 2505

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RESULT 14

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US-09-235-451-33
; Sequence 33. Application US/09235451
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.
; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
; CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
; POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 9076/084CIP
; CURRENT APPLICATION NUMBER: US/09/235,451
; CURRENT FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 2544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)...(2530)

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; OTHER INFORMATION: Human VRI
US-09-235-451-33

Query Match 26.8%; Score 660.8; DB 3; Length 2544;
Best Local Similarity 61.1%; Pred. No. 4.8e-157;
Matches 1206; Conservative 0; Mismatches 732; Indels 36; Gaps 7;
QY 316 TTGACCGAGATCGGCTCTTCAATGCGGTCTCCGGGGTGTCCCGAGGATCTGGCTGGA 375
DB 350 TATGATCGCAGGAGTATCTTTGAAGCGTGTCTCAGAAATACCTGCCAGGATCTGGAGAGC 409
QY 376 CTTCCAGAGTACCTGAGCAAGACGACCAAGTACTCACCGACTCGGATACACAGAGGGC 435
DB 410 CTGCTGCTCTTCCTGCAAGAGCAAGAGCACTCACAGAACAGGATTCGAAGACCT 469
QY 436 TCCACAGGTAAGACGTGCTGATGAAGGCTGTGCTGAACCTTAAGACGCGAGTCAATGCC 495
DB 470 GAGCAGGGAAGACCTGTCTGCTGAAAGCCATGCTCNACTGCAAGGACAGACACC 529
QY 496 TGCATTTCTGCCATCTGCTGCAAGTGCACAGGGAATCTGGGCAATCTCAGCCCTCTGGTAAT 555
DB 530 ACCATCCCCCTGCTCTCTGAGATCGCGCGCAACCGACAGCCTGAAGGAGCTTGTCAAC 589
QY 556 GCCAGTGCACAGTACTATTACCGAGGCCACAGCGCTCTGCACATCGCCATTCGAGAG 615
DB 590 GCCAGCTACACGACAGCTACTACAAGGGCCACAGACACTGCACATCGCCATCGAGAGA 649
QY 616 AGGAGTCTGCAGTGTGTGAAGCTCTCTGTGGAGAAATGGGGCCAAATGTGCATGCCCGGCC 675
DB 650 CGCNAATGCCCTTGTGACCTCTCTGTTGGAGAACCGAGCAGACGTCCAGGCTGCGGCC 709
QY 676 TGGCGCGCTTTCTTCAGAAAGGCGCAAG---GACATGCTTTTATTTGGGTGAGTACCC 732
DB 710 CATGGGAGCTCTTTAAGAAACCAAGGGCGCTGGATTCTACTTTCTGGTGAATGCC 769
QY 733 CTCTCTTTGGCGCTTGCACCAAGCAGTGGATGCTGTGTAAGTACTCTCTGGAGAACCCA 792
DB 770 CTGTCTGCGCGCTGCACCAACAGCTGGGATCGTGAAGTTCCTGCTGCAAGAACTCC 829
QY 793 CACGAGCCCGCAGCTGCAAGGCCACTGACTCCAGGGCAACACAGTCTCTGCAATGCCCTA 852
DB 830 TGGCAGAGCGCGACATACAGCGCCAGGACTCGGTGGGCAACACGCTGCTGCACGCCCTG 889
QY 853 GTGATGATCTCGCAAACTCAGCTGAGAAATTTGCACTGTGTGACCGAGCATGTATGATGGG 912
DB 890 GTGGAGGTGGCCGACAAACAGCGCCGCAACACAGAAATTTGTGACGACATGTACAATGAG 949
QY 913 CTCTCTCAAGCTGGGGCCCGCTCTGCCCTACCGTGCAGCTTCGAGGACATCCGCAACCTG 972
DB 950 ATTCTGATCTGGGGCCAACTGCACCCGACCTGAAGCTGGAGGAGCTCAACCAAG 1009
QY 973 CAGGATCTCAGCTCTGAAGCTGGCGCCGCAAGAGGGCAAGATTCGAGATTTTCAGGCAC 1032
DB 1010 AAGGAATGACCGCTGGCTCTGGCAGCTGGGACCGGGAAGATCGGGCTTTGGGCTAT 1069
QY 1033 ATCTCTCAGCGGAGTT-----TTAGGACTGAGCCACTTTTCCGAAAGTTTCAAGG 1086
DB 1070 ATTTCTCAGCGGAGATTCAGGAGCCGAGTGCAGGCCACTGTCCAGGAAGTTTCAAGG 1129
QY 1087 TGTGCTATGGGCTGTCCGGGTGTGCTGTATGACCTGTGCTGTGGACAGCTGTGAG 1146
DB 1130 TGGGCTTACGGGCGCGTGCATCTCTCTGTATGACCTGTCTGCTGCACTCGACACTGGAG 1189
QY 1147 GAGAACTCAGTCTGGAGATCATTTGCCCTTTCAATTGCA---AGAGCCCGCACCGACACCGA 1203
DB 1190 AAGAACTCGTGTGGAGGTGATCGCTACAGCAGCAGCGAGACCCCTTAATCGCCAGCAG 1249
QY 1204 ATGGTCTTTTGGAGCCCTTGAAACAATCTGCTGAGCGGAAATGGGA---TCTGCTCATC 1260
DB 1250 ATGCTCTTGTGGAGCGCTGAAACCGACTCTCTGAGGACAAAGTGGGACAGATTCGTCAAG 1309
QY 1261 CCCAAGTCTCTTAAACTTCTGTGTAATCTGATCTACATGTTTCACTTTCCAGCGCTGTT 1320

DB 1310 CGCATCTTCTACTTCAACTTCTCTGGTCTACTGCTGTATCATGATCATCTTCCACATGGCT 1369
QY 1321 GCCTACCATACGCTTACCCTGAAGAGCAGCGCGCCCTCACTCACTGAAGCGGAGGTTGGA 1380
DB 1370 GCCTACTACAGGCC-----CGTGGATGGCTTGGCTCCCTTTAAGATGGAAGAACTGGA 1423
QY 1381 AACTCCATGCTCTGACGGGCCACATCCTTATCTCTGCTAGGGGGGATCTACCTCTCTCGT 1440
DB 1424 GACTATTTCCGAGTTACTTGGAGAGATCTCTGTGTGTAGGAGGAGTCTACTTCTTTTTC 1483
QY 1441 GGCACAGCTCTGTACTTCTGCGGGGCGCACAGTGTTCATCTGGATCTCTGTTCTAGACAGC 1500
DB 1484 CGAGGATTCAGTATTTCTGTCAGAGGCGCGCTCGATGAAGACCTGTTTGTGGACAGC 1543
QY 1501 TACTTTGAAATCCTCTCTCTGTTTCAGAGCCCTCTGCTCAAGTGTGTCCAGGTGCTGTGT 1560
DB 1544 TACAGTGAGATGCTTTCTTCTCTGAGTCACTGTTTCACTGCTGCCACCGTGGTGTGTAC 1603
QY 1561 TTTCTGGCCATCAGTGTGTACCTGCCCCCTGCTGTGTCTGCTGCTGTGTGGCTGGCTG 1620
DB 1604 TTACGCCACTCAAGAGTATGTGGCTTCATGGTATTTCTCCCTGGCCTTTGGGCTGGACC 1663
QY 1621 AACCTGCTTTTACTATACAGTGGCTTTCAGACACACAGGCACTTACAGTGTCTATGATCCAG 1680
DB 1664 AACATGCTCTACTACACCGCGGTTTCCAGACAGATGGGCACTCTATGCCGTCTATGATAG 1723
QY 1681 AAGGTCACTCTCGGGAACCTGCTGGCTTCTTCTGTATCTAATTAGTCTTCTTTTTCGGC 1740
DB 1724 AAGATGATCTCAGAGACCTGTGCGGTTTTCATGTTTGTCTAGCTCTCTTCTTGTTCGGG 1783
QY 1741 TTTCTGCTGAGCCCTGGTGGCTGAGCCAGCAGGAGGCTTTGGCGCCCGAAGCTCTCAGAGC 1800
DB 1784 TTTTCCACAGCGGTGTGTGACGCTGATTTGAAGACGGGAAGATGACTCTCCCTGCCGTCTGAG 1843
QY 1801 CCCAATGCCACAGAGTCACTGTCAGCGCCATGAGAGGAGACAGAGGACAGAGGCAACGGGGC 1860
DB 1844 TCCACGTC-----GCACAGGTGCGGGGCGCTCCCTGCAGGCCCCCGATAGC 1891
QY 1861 CAGTACAGGGGTATCTGGAAGCCTCTCTTGGAGCTCTTCAAAATTTCAACATTCGGCATGGGC 1920
DB 1892 TCTCAACAACAGCTGTACTTCCACCTGCTGGAGCTGTTCAAGTTCACCATCGGCATGGGC 1951
QY 1921 GAGCTGGCTTCCAGAGCAGCTGCACTTTCGCGGCATGCTGCTGCTGCTGCTGCTGCTG 1980
DB 1952 GACCTGGAGTTCACTGAGAACTATGACTTCAAGGCTGTCTTATCATCTCTGCTGCTGCTG 2011
QY 1981 TAGCTGCTCTCACTTACATCTCTGCTGCTCAACATGCTCTCATCGCCCTCATGAGCAGAGC 2040
DB 2012 TATGTAATTTCTACCTTACATCTCTGCTCAACATGCTCATCGCCCTCATGGGTGAGACT 2071
QY 2041 GTCAACAGTGTGCCCTGACAGCTGGAGCATCTGGAAGCTTGGAGCTGAGAGGCAATCTCTGTC 2100
DB 2072 GTCAACAGATGCCACAGAGAGCAGAAACATCTGGAAGCTGCAAGAGCCATCACCATC 2131
QY 2101 CTGGAGATGGAATGGCTATTGGTGTGCAGGAAGAAG---CAGCGGCGAGGTGTGATG 2157
DB 2132 CTGGAACGCGAAGAGCTTCTTAAAGTCAATGAGGAAGGCTTCCGCTCAGGCAAGCTG 2191
QY 2158 CTGACCGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGTGTGCTTTCAGGGTGGAG 2217
DB 2192 CTCGAGTGGGTACACACTTGTATGGAAGGAGCACTACCGGTGGTGTCTTTCAGGGTGGAC 2251
QY 2218 GAGGTGAATGGGCTTTCATGGGAGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2271
DB 2252 GAGGTGAATGGGACCTTGGAAACACCAACGTTGGGCACTATCAACAGGAAGACCGC 2305

RESULT 15
US-09-978-303-33
; Sequence 33, Application US/09978303
; Patent No. 6790629
; GENERAL INFORMATION:
; APPLICANT: Julius, David J.

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; APPLICANT: Caterina, Michael J.
; APPLICANT: Brake, Anthony J.
; TITLE OF INVENTION: Nucleic acid sequences encoding
; TITLE OF INVENTION: capsaisin receptor and capsaisin receptor-related
; FILE OF INVENTION: polypeptides and uses thereof
; FILE REFERENCE: UCAL084CON
; CURRENT APPLICATION NUMBER: US/09/978,303
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/235,451
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/072,151
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 08/915,461
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2544
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-978-303-33

Query Match      26.8%; Score 660.8; DB 4; Length 2544;
Best Local Similarity 61.1%; Pred. No. 4.8e-157;
Matches 1206; Conservative 0; Mismatches 732; Indels 36; Gaps 7;

Qy      316 TTTGACCGAGATCGGCTCTTCAATGCGGTCTCCGGGGTGTCCCGAGGATCTGGCTGGA 375
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      350 TATGATCGCAGGAGTATCTTTGAAGCCGTTGCTCAGAAATACTGCCAGGATCTGGAGAGC 409
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      376 CTTTCCAGAGTACCTGAGCAAGACAGCAAGTACTCTACCGACTCGGAATACACAGAGGGC 435
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      410 CTGCTGCTCTTCTTCGAGAGAGCAAGACCTCTACAGACAGAGTTCAAGACCCT 469
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      436 TCCACAGGTAAAGCTGCTGATGAAGCTGTGCTGAACCTTAAGGACGGAGTCAATGCC 495
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      470 GAGACGGAGAGACCTGTCTGCTGAAAGCCATGCTCAACCTGACAGCAGCAGACCAACC 529
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      496 TGAATCTGCCACTGCTGAGATCGACAGGACTCTGGCAATCTCTAGCCCTCTGGTAAAT 555
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      530 ACCATCCCTCTCTCTCGAGATCGCGCGCAACCGGACACCTTGAAGGAGCTTGTCAAC 589
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      556 GCCCAGTGCAAGATGACTATTACCGAGGCCACAGCGCTCTGCACATCGCCATTGAGAAG 615
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      590 GCCAGCTACCGGACAGCTACTCAAGGCCACAGACACTGACACATGCGCATCGCCATGAGA 649
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      616 AGGAGTCTGCAGTGTGTGAAGCTCTCTGTTGAGAAATGGGCAATGTGCATGCCCGGCC 675
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      650 CGCAACATGGCCCTGGTGACCTCTCTGTGAGAAACGAGCAGACGCTCCAGGCTGCGGCC 709
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      676 TGGCGCGCTTTCTTCAGAGAGGGCCAG---GGACTTGTCTTTTATTTCGGTGAGCTACCC 732
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      710 CATGGGACTTCTTTAAGAAACCAAGGGCGGCTGGAATTCTACTTTCGGTGAATCGCC 769
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      733 CTCTCTTTGGCGCTTGACCAAGCAGTGGGATGTTGTTAAGCTACCTCTCTGGAGAACCCA 792
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      793 CACCAGCCCGCAGCTGCAAGCCACTGACTCCAGGGGCAACACAGCTCTGSCATGCCCTA 852
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      830 TGGCAGAGCGGACATCAGCGCCAGGGACTCGGTGGGCAACACGGTGTGCACGCCCTG 889
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      890 GTGAGGTGGCGGCAACACCGCGCCGACAAACGAAAGTTTGTGACGAGCATGTACAATGAG 949
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      913 CTCCTCAAGCTGGGCGCGCTCTGCCCTACCGTGCAGCTTGAAGACATCCGAACCTG 972
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      950 ATTCTGATCTGGGGGGGCAAACTGCAACCCGACGCTGAAGCTTGAAGAGCTCACCACAG 1009
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      973 CAGGATCTCAGGCTCTGAAGCTGGCGCGCCAGGAGGGCAAGATCGAGATTTTCAGGCAC 1032
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1010 AAGGAATGACGCCGCTGGCTCTGGCAGCTGGGACCTGGGAGCAAGAACTCTGGAGGCTGCAGAGGCCATCACCATC 1069
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy      1033 ATCTGTCAGCGGAGTT-----TTCAGGACTGAGCCACCTTTTCCGAAAGTTTCCCGAG 1086
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1070 ATTTCCACGGGAGATCAGGAGCCGAGTGCCAGGACCTGTCCAGGAAGTTTCCCGAG 1129
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1087 TGGTGTATGGGCTGTGCGGGTGTGCGTGTATGACCTGGCTTCTGTGACAGCTGTGAG 1146
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1130 TGGGCTTACGGGCGGTGCACTCTCGCTGTACGACCTGTCTGTCGACAGCTTCCGAG 1189
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1147 GAGAACTCAGTCTGAGATCATTTGCTTTTCAATTGCA---AGAGCCCGCACCCGACACCGA 1203
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1190 AAGAACTCGGTCTGGAGGTGATCGCTACAGCAGCAGCGAGACCCCTTAATCGCCAGC 1249
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1204 ATGGTCTGTTTGGAGCCCTGAAACAACTGCTGACGGCGAAATGGGA---TCTGTCTCATC 1260
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1250 ATGCTCTTGTGGAGCCGCTGAACCGACTCTGCGAGCAAGTGGGACAGATTCGTCAAG 1309
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1261 CCCAAGTCTCTTAAACTTCTGTGTATCTGATCTACATGTTCATCTTCACCGCTGTT 1320
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1310 CGCATCTTCTACTTCAACTTCTGCTGTATGCTGTATCATGATCATCTTTTCCCATGGCT 1369
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1321 GCCTACCATCAGCTACCTCTGAAGAGCAGGCGCGCCCTCACCTGAAAGCGGAGGTGGA 1380
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1370 GCCTACTACAGGCC-----CGTGGATGGCTTGCCTCCCTTTAAGATGGAATAAACTGGA 1423
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1381 AACTCCATGCTGTGACGGGCCCATCTTTATCTCTGTAGGGGGATCTACCTCTCTCGTG 1440
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1424 GACTATTTCCGAGTTACTGGAGAGATCTGTCTGTGTGTAGGAGGAGTCTACTTCTTTTTC 1483
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1441 GGCACGCTGTGTACTTTCTGCGCGCGCAGTGTTCATCTGGATCTCGTTTCATAGACAGC 1500
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1484 CGAGGATTCAGTATTTCTCTGCAGAGCGCGCTCGATGAAGACCCCTGTTTGTGGACAGC 1543
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1501 TACTTTGAAATCTCTTCTGTTTCCAGGCCCTGCTCACAGTGTGTCCAGGTGCTCTGT 1560
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1544 TACAGTGAGATGCTTTCTTCTTGCAGTCACTGTTTATGCTGGCCACCGTGGTGTCTGAC 1603
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1561 TTCTCGGCCATCAGTGTGTACCTGCTTGTGTGTCTGCTGTGTGTGTGGGTGGGTGCTG 1620
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1604 TTACAGCACTCAAGGATATGTGGCTTCCATGTTATTTCTCTCTGGCTTGGGCTGAGCC 1663
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1621 AACCTGCTTTATATACATGCTGCTTCCAGCACACAGGCACTTACAGTGTCTATGATCCAG 1680
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1664 AACATGCTCTACTACACCCCGCGTTCACAGCAGATGGGCATCTATGCGGCTCATGATAGAG 1723
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1681 AAGGTCACTCTGCGGAGACCTGCTGCTTCTGATCTACTTTAGTCTTCTCTTTTCGGC 1740
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1724 AAGATGATCTGAGAGACCTGTGCCGTTTCTATGTTTGTCTACGTCGTTCTTCTTCTGGG 1783
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1741 TTGCTGTAGCCCTGTGTGAGCTGTGAGCCAGGAGGCTTTGGCGCCCGCCGAAAGCTCTTACAGGC 1800
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1784 TTTTCCACAGCGGTGGTGACGCTGATTGAAGACGGGAAGAAATGACTCCCTGCGCTCTGAG 1843
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1801 CCCAATGCCACAGATCAGTGACGCCCATGGAGGACAGAGGACGAGGGGCAAGCGGGCC 1860
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1844 TCCACGTC-----GCACAGGTGGCGGGGCTGCTGTCAGGCGCCCGCATAGC 1891
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1861 CAGTACAGGGGTATCTCGGAAGCCTCTCTGAGCTCTTCAAAATTCACCATCGGATGGGC 1920
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1892 TCCTTACAAAGCCTGTATCTCACCTGCTGAGCTGTTCAAGTTTCAATCGGCAATGGGC 1951
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1921 GAGCTGGCTTCCAGGAGCAGCTGCACTCTCGCGGCAATGGTGTCTGTCTGTCTGTCTG 1980
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1952 GACTGAGTTCACTGAGAACTATGACTTCAAGGCTGTCTTTCATCATCTCTGTCTGTG 2011
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1981 TACGTGCTGTCTACCTTACATCTGTCTCAATGTCTATGCGCCCTCATGAGCGAGACC 2040
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      2012 TATGTAATTTCTACCTACATCTCTCTCAACATGCTCATCGCCCTCATGGGTGAGACT 2071
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      2041 GTCAACAGTGTCCCACTGACGCTGGAGCATCTGGAAGCTGCAAGAAGCCATCTCTGTCT 2100
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      2072 GTCAACAGATTCGCAAGGAGCAAGAACTCTGGAAAGCTGCAAGAGGCCATCACCATC 2131
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY	2101	CTGGAGATGAGAAATGGCTATTGGTGTGTCAGGAAGAAG---CAGCGGGCAGGTGTGATG	2157
Db	2132	CTGGACACGGGAGAAAGAGCTTCCTTAAGTGCATGAGGAAGGCCCTTCGCTCAGGCAAGCTG	2191
QY	2158	CTGACCGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGGTGTCTTCAGGGTGGAG	2217
Db	2192	CTGCAGGTGGGTACACACCTGATGGCAGGACGACTACCGTGGTGTCTTCAGGGTGGAC	2251
QY	2218	GAGGTGAACCTGGGCTTTCATGGGAGCAGACGCTGCCTACGCTGTGTGAGGACCCG	2271
Db	2252	GAGGTGAACCTGGACCACTGGAACACCAACGTGGGCATCATCAACGAAGACCCG	2305

Search completed: October 6, 2005, 22:59:28
Job time : 441 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 17:19:16 ; Search time 7208 Seconds
(without alignments)
13038.385 Million cell updates/sec

Title: US-09-445-614B-1

Perfect score: 2469

Sequence: 1 cagcaggcgcagcgcagct.....gctggctcggggctccagct 2469

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hic.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_ges1.*
- 9: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1581.2	64.0	2760	3 AK089004	AK089004 Mus muscu
2	1505.8	61.0	2270	3 AK008689	AK008688 Mus muscu
3	884.6	35.8	962	5 BQ652688	BQ652688 AGENCOURT
4	871.6	35.3	933	5 BQ678083	BQ678083 AGENCOURT
5	866	35.1	940	5 BQ645005	BQ645005 AGENCOURT
6	851.2	34.5	902	5 BQ650623	BQ650623 AGENCOURT
7	850	34.4	907	5 BQ653925	BQ653925 AGENCOURT
8	849.2	34.4	945	5 BQ643665	BQ643665 AGENCOURT
9	829.2	33.6	871	5 BQ644508	BQ644508 AGENCOURT
10	819.8	33.2	1009	5 BQ644773	BQ644773 AGENCOURT
11	809.6	32.8	870	4 BQ743115	BQ743115 602634253
12	804.6	32.6	862	5 BQ838779	BQ838779 AGENCOURT
13	795.2	32.2	3674	3 AK038307	AK038307 Mus muscu
14	793.6	32.1	915	5 BQ838756	BQ838756 AGENCOURT
15	786	31.8	941	5 BQ653113	BQ653113 AGENCOURT
16	778	31.5	922	5 BQ643949	BQ643949 AGENCOURT
17	775	31.4	957	5 BQ644054	BQ644054 AGENCOURT
18	772.2	31.3	880	4 BQ764899	BQ764899 602737335
19	754.2	30.5	785	4 BQ765155	BQ765155 602737587
20	744.8	30.2	951	4 B1819175	B1819175 603036979
21	705.2	28.6	886	5 BQ644271	BQ644271 AGENCOURT
22	693.4	28.1	976	5 BQ679954	BQ679954 AGENCOURT
23	691.8	28.0	753	6 CD365397	CD365397 UI-H-FT2-
24	690.4	28.0	751	6 CA432218	CA432218 UI-H-FG1-

25	688.6	27.9	793	1 AU141855	AU141855 AU141855
26	685.8	27.8	926	6 CD513620	CD513620 AGENCOURT
27	676.6	27.4	757	5 BU617949	BU617949 UI-H-DF0-
28	675.8	27.4	756	4 BM007978	BM007978 603617714
29	670.6	27.2	742	6 CB528322	CB528322 UI-H-FT2-
30	662.6	26.8	753	5 BX339344	BX339344 BX339344
31	662.4	26.8	4187	3 HSM801769	AL136801 Homo sapi
32	662	26.8	711	7 CN480858	CN480858 UI-H-FT2-
33	660.6	26.8	712	6 CD627522	CD627522 55109895H
34	651.4	26.4	953	4 BG254423	BG254423 602369021
35	644.4	26.1	901	5 BU190985	BU190985 AGENCOURT
36	630.2	25.5	686	2 AW976725	AW976725 EST388834
37	629.8	25.5	896	5 BU540815	BU540815 AGENCOURT
38	625	25.3	625	7 CV027855	CV027855 6217 Full
39	622.4	25.2	970	5 BQ888238	BQ888238 AGENCOURT
40	596.2	24.1	682	2 BF732920	BF732920 nael7b01.
41	588	23.8	588	2 BF940288	BF940288 7043F06.X
42	585	23.7	585	5 BP304605	BP304605 BP304605
43	580.2	23.5	872	4 BG765286	BG765286 602738720
44	578.4	23.4	616	1 AI801897	AI801897 tx28h02.X
45	577.4	23.4	632	5 BU632884	BU632884 UI-H-FE1-

ALIGNMENTS

RESULT 1

AK089004

LOCUS

DEFINITION

AK089004 2760 bp mRNA linear HTC 03-APR-2004
Mus musculus 2 days neonate thymus thymic cells CDNA, RIKEN
full-length enriched library, clone:B430035F12 product:vanilloid
receptor-like protein 1, full insert sequence.

ACCESSION

AK089004

VERSION

AK089004.1 GI:26354129

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus

ORGANISM

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

PUBMED

10349636

REFERENCE

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

PUBMED

11042159

REFERENCE

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

PUBMED

11076861

REFERENCE

4

The RIKEN Genome Exploration Research Group Phase II Team and the

PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

The FANTOM Consortium and the RIKEN Genome Exploration Research

1319	AGCGGAGTTCTCAGGGCTGTACAGGCCCTTTCCGAAAGTTACCGAGTGGTGCTACG	1376
1097	GGCTCTCGCGGTGTGCGCTGTATGACCTGGCTTCTGTGGACAGCTGTGAGGAACTCAG	1156
1379	GTCTGTCCGAGTGTCACTGTATCGACCTGTCTCTGTGGACAGCTGGGAAAGAACTCGG	1438
1157	TGCTGAGATCATTTGCTTTTCATTTGCNAGAGCCGACACGACACCGAATGGTTCGTTTGG	1216
1439	TTCTGGAATCATTCGCTTTCCATTTGCAAGAGCCGACACCGGACCCGATGGTGGTTTTAG	1498
1217	AGCCCTTGAACAACTGCTCAGCGCAAAATGGGATCTGCTCATCCCCAAGTCTTCTTAA	1276
1499	AGCCACTGAACAAAGTTCTGCAGAGAAATGGGATCGGCTCATCCCAGAATCTTCTTCA	1558
1277	ACTTCTGTGTAATCTGATCATATGTTTCATCTTTACCCGCTGTGTGCTACCATCAGCCTA	1336
1559	ACTTCGCCTTACTTGGTCTCATATGATCATCTTACCATAGTTGGCTACCCACGAGCTT	1618
1337	CCCTGAAGAAAGAGCGGCCCTTCACCTGAAGCGGAGGTTTGAACACTCATCTGCTGTA	1396
1619	CCCTGGAGCAGCAGCAATTCCTCTCATCAAAGCGAATTTTGGGGAATCCATCTGCTGT	1678
1397	CGGGCCACATCTTATCTGCTAGGGGGATCTACCTCTCCTGCGGGCCAGCTGTGGTACT	1456
1679	TGGGCCACATTCATGATCCTCTCTGGGGATTTTACCTCTTACTTGGGCCAGCTGTGGTACT	1738
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1799	TCCTTGTCCAGGGCGTCTCACAGTGTGTCCTCCAGGTGCTCGCTTCGTGGAGACTGAAT	1858
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1859	GSTACCTCCCCCTGTTAGTGATCATCCCTATGTGCTGGGCTGGCTGTAATTTATATA	1918
1637	CAGTGGCTTCCAGCACACAGGCAATCPACAGTGTCTATGATCCAGAAAGTTCATCCTGCGGG	1696
1919	CAGTGGCTTTACGACACACAGGCATCTACAGTGTCTATGATCCAAAGGTCAATCTGCGAG	1978
1697	ACCTGTGCGCTTCCTTCTGATCTACTTATGTCTCTTTTCGGTTCGCTGTAGCCCTGG	1756
1979	ACCTGCTCCGCTTCTCTGCTGTCTACCTAGTCTCTCTTTTCGGCTTTCGTGTAGCCCTAG	2038
1757	TGAGCTTGAGCAGGAGCTTGGGCCCCGNAAGTCTCTACAGGCCCAATGCCACAGAT	1816
2039	TAAAGTTTGAACCGGAGCCCGAAGTCCCAAGGCCCTGAAAGATAGCAACACCACTGTGA	2098
1817	CAGTGCAGCCCATGAGGGGACAGAGGACAGAGGCAACGGGGCCAGTACAGGGGTATCC	1876
2099	CGGAAAGCCCA CGCTGGTTCAGAGAGGAGGCC- - - - -AGTCCCATATGGGGGCATTC	2152
1877	TGGAAGCCTCCTTTGGAGCTCTTCAAATTCACCATCGGCATGGGCGAGCTGGCCTTCCAGG	1936
2153	TGGATGCTCCCTTAGAGCTGTTCAAGTTACCAATGGGTATGGGTGAGCTGGCTTTCAGG	2212
1937	AGCAGCTGCATTCGCGGCCATGTGTGCTGTCTGTGCTGGCCCTACGTGCTGCTCACTT	1996
2213	AACAGCTGCGCTTTTGTGGGGTGGTGTGCTGTGTTGCTGTGTTGGCCCTACGTCTCTCACTT	2272
1997	ACATCTGTGCTCAACATGCTCATCGCCCTCATGAGCGAGACCGTCAACAGTGTGCGCA	2056
2273	ACGTCTACTGCTCAACATGCTCATTTGCCCTCATGAGTGAACCTGTCAACAGCGTTGCCA	2332
2057	CTGACAGCTGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCTCTGGAGATGGAGAATG	2116
2333	CTGACAGCTGAGCATCTGGAAGTTGCAGAAAGCCATCTCTGTCTTGGAGATGGAGAATG	2392
2117	GCTATTTGGTGTGACGGAGAA- - - - -GCMGCGGCGAGGTGTGATCTGACCGTTGGCACTA	2173
2393	GTTACTGTGTGTGAGAGGAAAGGCAATCCGACGAGGAGCTCTGTAAAGTTGGCACTA	2452

QY	2174	AGCCAGATGCGAGCCCGGATGAGGGCTGGTGGCTTCAAGGTGGAGGAGGTGCACTGGGCTT	2233
Db	2453	AAGGGGATGTGTATACCTGATGAGCGCTGGTGGCTTCAAGGTGGAGGAAGTAACTCTGGGCTG	2512
QY	2234	CATGGGAGCAGACGCTCCCTACGCTGTGTGAGGACCCGTCAGGGCGAGGTGTCCCTCGAA	2293
Db	2513	CATGGGAGAGACCTTCCACCTTATCTGAGGATCCATCAGGGCGAGGCATCACTGGTT	2572
QY	2294	CTCTCGAGAACCCGTCTCGGCTTCCCTCCCAAGGAGGATGAGGATGTGGCTCTCAGG	2353
Db	2573	ATAAAAGAACC-----CAACCTCTAACTGGGAAGAACAGTGCCTCTCAGAGG	2620
QY	2354	AAACTATGTGCCGTCCAGTCTCTCCAGTCCCACTCATGCCCCAGATGCAGCAGGA---	2410
Db	2621	AAGACCAATCTGCCTCTTTCAGGTCTCCAGTCTCCACTGCATGCGTCCAGATGGCGACGACCA	2680
QY	2411	-GGCCAGAGGACAGAGCAGAGGATCTTTTCCAAACCACTCTGCTGGCTCTG	2459
Db	2681	GGTGGCAGAGGTACAGTATAGGAAATTTTTCAGCCAGCCACACCCGAGGCTACTG	2730

RESULT 2

AK008689	2270 bp	mrna	linear	HTC 03-APR-2004
LOCUS				
DEFINITION	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210009M20 product:vanilloid receptor-like protein 1, full insert sequence.			
ACCESSION	AK008689			
VERSION	AK008689.1	GI:12843037		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiyake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			
MEDLINE	20530913			
PUBMED	11076861			
REFERENCE	4			
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature 409, 685-690 (2001)			
REFERENCE	5			
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.			
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs			
JOURNAL	Nature 420, 563-573 (2002)			

1332 GTGCTGTCCAGGTGCTGGCTTTCGTGGAGACTGAATGGTACCTCCCTGTTAGTGTCA 1391
 QY 1600 GCGCTGGTCTGGCTGGCTGAACCTGCTTTACTATACAGCTGGCTTCCAGCACACAGGC 1659
 Db 1392 TCCTTAGTGTGGCTGGCTGAACCTGCTTTATATACAGCTGGCTTCCAGCACACAGGC 1451
 QY 1660 ATCTACAGTGTCAATGATCAGAAAGGTCACTCTCGGGAGCTGTGCGCTTCTTCTGATC 1719
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 QY 1840 GAGGACGAGGCAACCGGGCCAGTACAGGGGTATCTTGGAGCTCTTGGAGCTCTTC 1899
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 Db 1806 ATTGCCCTCATGATGAGCTGTCAACAGGTTGGCACTGAGCTGAGCTGAGCTGAG 1865
 QY 2080 CTCGAGAAAGCCATCTCTGCTGAGAGTGGAGATGGCTATTGGTGGTGCAGAGAGAA- 2138
 Db 1866 TTGCAGAAAGCCATCTCTGCTGAGAGTGGAGATGGCTATTGGTGGTGCAGAGAGAA 1925
 QY 2139 --GCAGGGGAGGTGATGCTGACCGTTGGCACTTAAGCCAGATGCGACCGCGATGAG 2196
 Db 1926 AGGCATCGCGAGGAGGCTGCTGAAAGTTGGCAACAAAGGGATGGTATATCTGATGAG 1985
 QY 2197 CGCTGGTGTCTCAGGGTGGAGAGGTGAACCTGGCTTTCATGGAGCAGAGCGCTGCTACG 2256
 Db 1986 CGCTGGTGTCTCAGGGTGGAGAGGTGAACCTGGCTTTCATGGAGCAGAGCGCTGCTACG 2045
 QY 2257 CTGTGTGAGAACCGTTCAGGGGAGGTGTCCCTCGAACTCTCGAGAAACCTGTCTGGCT 2316
 Db 2046 TTATCTGAGGATCCATCAGGGGAGGCTCACTGGTTTATAAAAGAAC----- 2094
 QY 2317 TCCCTCCAGAGGATGAGATGGTGTCTCTGAGGAAACTATGTGCCGCTCCAGCTC 2376
 Db 2095 -CAACTCTAACTCTGGAAGAGACAGTGGCTTCAGAGGAGAACCACTGCTCTTCAGGTC 2153
 QY 2377 CTCAGTCCCACTGATGCGCCAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2432
 Db 2154 CTCAGTCCCACTGATGCGCCAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2213
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 Db 2214 TTTTCCAGGACACCCGAGGCTACTG 2240

RESULT 3
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 LOCUS
 DEFINITION AGENCOURT 8492955 NIH_MGC_100 Homo sapiens cdna clone IMAGE:6300205
 5', mRNA sequence.
 BQ652688
 VERSION BQ652688.1 Gi:21776860
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 962)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2514 row: b column: 14
 High quality sequence stop: 632.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /tissue_type="hepatocellular carcinoma, cell line"
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 /clone_lib="NIH MGC 100"
 /note="Organ: liver; Vector: pOTB7; Site: 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

ORIGIN

Query Match 35.8%; Score 884.6; DB 5; Length 962;
 Best Local Similarity 96.9%; Pred. No. 2.6e-202;
 Matches 932; Conservative 0; Mismatches 27; Indels 3; Gaps 3;
 QY 1483 ATCTGTTTATGACAGCTACTTTGAAATCCTTCTGTTTCCAGGCCCTGCTCACAGTG 1542
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 QY 1543 GTGTCCAGGTGTGTTTCTGTCATCGAGTGGTACCTGCTGCTGCTGCTGCTGCTGCTG 1602
 Db 61 GTGTCCAGGTGTGTTTCTGTCATCGAGTGGTACCTGCTGCTGCTGCTGCTGCTGCTG 120
 QY 1603 CTGCTGCTGGCTGGCTGAAACCTGCTTACTATACAGTGGCTTCCAGCACACAGGATC 1662
 Db 121 CTGCTGCTGGCTGGCTGAAACCTGCTTACTATACAGTGGCTTCCAGCACACAGGATC 180
 QY 1663 TACAGTGTATGATCCAGAGGTATCTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1722
 Db 181 TACAGTGTATGATCCAGAGGTATCTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 1723 TTAGTCTTCTTTTGGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 1782
 Db 241 TTAGTCTTCTTTTGGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 300
 QY 1783 CCGAAGCTCTTACAGCCCCCAATGCCACAGAGTCACTGACAGGAGGCTTGGCGC 1842
 Db 301 CCGAAGCTCTTACAGCCCCCAATGCCACAGAGTCACTGACAGGAGGCTTGGCGC 360
 QY 1843 GACAGGCGCAACCGGGCCAGTACAGGGGTATCTTGAAGCTCTTGGAGCTTCTTCAA 1902
 Db 361 GACAGGCGCAACCGGGCCAGTACAGGGGTATCTTGAAGCTCTTGGAGCTTCTTCAA 420
 QY 1903 TTTCCATCGGATGGCGAGCTGGCTTCCAGGAGCAGCTGCACTTCCCGGCGATGGT 1962
 Db 421 TTTCCATCGGATGGCGAGCTGGCTTCCAGGAGCAGCTGCACTTCCCGGCGATGGT 480

Matches	840;	Conservative	0;	Mismatches	14;	Indels	2;	Gaps	2;
QY	1490	TCATAGACAGCTACTTTGAAATCCTCTTCTGTTTCAGAGCCCTGCTCACAAGTGGTGTCCC	1549						
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QY	1550	AGGTGCTGTGTTTCTCGGCATCGAGTGGTACCTGCCCTGCTGTGCTGCGCTGCTGC	1609						
Db	62	AGGTGCTGTGTTTCTCGGCATCGAGTGGTACCTGCCCTGCTGTGCTGCGCTGCTGC	121						
QY	1610	TGGGCTGGCTGAACCTGCTTTTATATACACGTCGGCTTTCAGACACACAGGCACTACAGTG	1669						
Db	122	TGGGCTGGCTGAACCTGCTTTTATATACACGTCGGCTTTCAGACACACAGGCACTACAGTG	181						
QY	1670	TCATGATCCAGAAAGGTGATCCTCGCGGACCTGCTGCGCTTCTCTGATCTACTTAGTCT	1729						
Db	182	TCATGATCCAGAAAGGTGATCCTCGCGGACCTGCTGCGCTTCTCTGATCTACTTAGTCT	241						
QY	1730	TCCTTTTCGGCTTCGGCTGAGCCCTGGTGAGCCTGAGCCAGGAGGCTTGGCGCCCGAAG	1789						
Db	242	TCCTTTTCGGCTTCGGCTGAGCCCTGGTGAGCCTGAGCCAGGAGGCTTGGCGCCCGAAG	301						
QY	1790	CTCTACAGGCCCCAAATGCCACAGAGTCAGTCAGAGCCCATGGAGGACAGAGGAGG	1849						
Db	302	CTCTACAGGCCCCAAATGCCACAGAGTCAGTCAGAGCCCATGGAGGACAGAGGAGG	361						
QY	1850	GCAACGGGGCCAGTACAGGGGTATCTGGAAGCTTCTTGGAGCTTCTCAAAATTACCA	1909						
Db	362	GCAACGGGGCCAGTACAGGGGTATCTGGAAGCTTCTTGGAGCTTCTCAAAATTACCA	421						
QY	1910	TCCGCAATGGCGAGCTGGCTTCCAGGAGCAGCTGACATTCCTCCGCGCATGCTGCTGC	1969						
Db	422	TCCGCAATGGCGAGCTGGCTTCCAGGAGCAGCTGACATTCCTCCGCGCATGCTGCTGC	481						
QY	1970	TGCTGCTGGCTACGCTGCTCTCACCTACATCTGCTGCTCAACATGCTCATCGCCCTCA	2029						
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QY	2030	TGAGCGAGACCGTCAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTCGAAG	2089						
Db	542	TGAGCGAGACCGTCAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTCGAAG	601						
QY	2090	CCATCTCTGCTGGAGATGGAAATGGCTATTTGGTGTGTCAGAGAGACAGCGGGCAG	2149						
Db	602	CCATCTCTGCTGGAGATGGAAATGGCTATTTGGTGTGTCAGAGAGACAGCGGGCAG	661						
QY	2150	GTGTGATGCTGACCG-TTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGGTCTTC	2208						
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QY	2209	AGGTGGAGAGGTGAATCGGCTTCATGGAGACAGCGTGCCTA-CGCTGTGTGAGGA	2267						
Db	722	AGGTGGAGAGGTGAATCGGCTTCATGGAGACAGCGTGCCTA-CGCTGTGTGAGGA	781						
QY	2268	CCGCTCAGGGGAGGTGCTCCTCGAACTCTCGAGAACCTGCTGCTGCTCCCTCCCA	2327						
Db	782	CCGCTCAGGGGAGGTGCTCCTCGAACTCTCGAGAACCTGCTGCTGCTCCCTCCCA	841						
QY	2328	GGAGGATGAGGATGGT 2343							
Db	842	GGATGAGATGGTGTCT 857							

RESULT 12
 BU838779
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BU838779
 AGENCOURT_8210115 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6258039
 5', mRNA sequence.
 BU838779
 BU838779.1 GI:24023174
 EST.
 Homo sapiens (human)
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NIH-MGC http://mgc.hci.nih.gov/.	
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	
Contact: Robert Strausberg, Ph.D.	
Email: cgapbs-r@mail.nih.gov	
Tissue Procurement: DCTD/DTF	
cDNA Library Preparation: Rubin Laboratory	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Agencourt Bioscience Corporation	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
Plate: LLCM2413 row: e column: 16	
High quality sequence stop: 653.	
Location/Qualifiers	
1. 862	
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/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="IMAGE:6258039"	
/tissue_type="melanotic melanoma, cell line"	
/lab_host="DH10B (phage-resistant)"	
/clone_lib="NIH MGC 112"	
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	
Query Match	32.6%; Score 804.6; DB 5; Length 862;
Best Local Similarity	98.9%; Pred. No. 5.2e-183;
Matches	842; Conservative 0; Mismatches 4; Indels 5; Gaps 3;
QY	1191 GCACCGACACCGAATGGTCTGTTTGGAGCCCTCGAACAACTGCTGCGAGCGAAATGGGA 1250
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QY	1251 TCTGTCTATCCCCAAGTCTTCTTAAACTCTCTGTGTATCTGATCTATCTTCTTCTT 1310
Db	60 TCTGTCTATCCCCAAGTCTTCTTAAACTCTCTGTGTATCTGATCTATCTTCTTCTT 119
QY	1311 CACCGCTGTTCCTACCATCAGCTACCTCGAAGAGCAGCGCCGCTCACCTGAAAGC 1370
Db	120 CACCGCTGTTCCTACCATCAGCTACCTCGAAGAGCAGCGCCGCTCACCTGAAAGC 176
QY	1371 GGAGGTGGAAACTCCATCTGCTGACGGGCCACATCTCTTATCTCTGTAGGGGGGATCTA 1430
Db	177 GGAGGTGGAAACTCCATCTGCTGACGGGCCACATCTCTTATCTCTGTAGGGGGGATCTA 236
QY	1431 CCTCTCTGTGGCCAGCTGTGTACTTCTGGGGGCCACGTTTCTGATCTCTGATCTCGTT 1490
Db	237 CCTCTCTGTGGCCAGCTGTGTACTTCTGGGGGCCACGTTTCTGATCTCTGATCTCGTT 296
QY	1491 CATAGACAGCTACTTTTGAATCTCTTCTCTGTTTCCAGGCCCTGCTCACAGTGTGTCCCA 1550
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QY	1551 GGTGTGTGTCTTCTGGCCATCGAGTGGTACTTGGCCCTGCTGTGTGTGTGTGTGTGTGT 1610
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QY	1611 GGGCTGGCTGAACCTGCTTTTATATACAGTGGCTTCCAGCACACAGGATCTTACAGTGT 1670
Db	417 GGGCTGGCTGAACCTGCTTTTATATACAGTGGCTTCCAGCACACAGGATCTTACAGTGT 476
QY	1671 CATGATCCAGAAAGGTCTATCTGCGGACCTGCTGCGCTTCTTCTGATCTTACTTCTT 1730

REFERENCE
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Db	477	CATGATCCAGAGGTCTCTCGGACCTGCTGGCTTCTCTGATCTACTTACTGCTT	536
Qy	1731	CCTTTTCGGGTTTCGCTGTAGCCCTGTGTAGCCCTGTGAGCGAGGCTTGGGGCCCCGAAGC	1790
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VERSION BU838756.1 GI:24023151
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ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DP
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (ILLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.llnl.gov
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/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
ORIGIN
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Matches 860; Conservative 0; Mismatches 14; Indels 8; Gaps 5;
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JOURNAL
COMMENT

FEATURES
Source

[illegible][illegible]

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REFERENCE	<p>1 (bases 1 to 941)</p>
AUTHORS	<p>NIH-MGC http://mgc.nci.nih.gov/.</p>
TITLE	<p>National Institutes of Health, Mammalian Gene Collection (MGC)</p>
JOURNAL	<p>Unpublished (1999)</p>
COMMENT	<p>Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov Tissue Procurement: CGAP (Stanford) cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L12CM2447 row: f column: 06 High quality sequence stop: 725.</p>

FEATURES

ORIGIN

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Best Local Similarity	94.5%;	Pred. No. 1.6e-178;		
Matches 869;	Conservative 0;	Mismatches 39;	Indels 12;	Gaps 5;
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DB	1	ATCTCGTTTCATAGACAGCTACTTTTGAATACCTCTTCTCTGTTCCAGGCCCTTGCTCACAGTG	60	
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QY	1903	TTCCATTCGCGCATGGCGAGCTGGCCCTTCCAGSAGCAGCTGCATCTTCCGGGAGTGGT	1962	
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Job time : 7219 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 14:22:24 ; Search time 1224 Seconds
(without alignments)
11941.047 Million cell updates/sec

Title: US-09-445-614B-1

Perfect score: 2469
Sequence: 1 cagcagccgacgcagctc.....gctgctcggggtccagct 2469

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2462.2	99.7	2809	13 Adq89073	Adq89073 Human uro
5	2460.6	99.7	2774	13 Adq83962	Adq83962 Human tum
6	2460.6	99.7	2807	13 ADP25060	Adp25060 PRO polyt
7	2455.8	99.5	2825	4 AAD09554	Aad09554 Human tra
8	2447.4	99.1	2867	6 ABL09839	Ab190839 Human pol
9	2444.6	99.0	2783	2 AAZ22829	Aaz22829 Human van
10	2428.8	98.4	2765	3 AAA14874	Aaa14874 DNA encod
11	2424.6	98.2	2805	6 ABX04237	Abx04237 Human cdn
12	2424.6	98.2	2805	9 ACD91294	Ac91294 Human van
13	2397.8	97.1	2507	12 ADP09695	Adp09695 Human VRL
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15	2347.8	95.1	2351	2 AAZ07114	Aaz07114 Human van
16	2333.4	94.5	2348	2 AAZ07116	Aaz07116 Human van
17	2293.4	92.9	2295	12 ADI81597	Adi81597 Human van
18	2263.2	91.7	2295	12 ADI81599	Adi81599 Human van
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21	2259.2	91.5	2779	9 ACD82821	Ac82821 cDNA sequ
22	2259.2	91.5	2779	10 ADI22906	Adi22906 cDNA enco
23	2259.2	91.5	2779	12 ADH73908	Adh73908 Human sec
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25	2061.8	83.5	2860	6 ABS73801	Ab573801 Human cdn
26	2061.8	83.5	2860	9 ACD82944	Ac82944 cDNA sequ
27	2061.8	83.5	2860	10 ADH73029	Adh73029 cDNA enco
28	2061.8	83.5	2860	12 ADH74031	Adh74031 Human sec
29	1933.4	78.3	1935	12 ADI81573	Adi81573 Human van
30	1720	69.7	1790	6 ABS70410	Ab570410 Human bon
31	1535.8	62.2	2271	12 ADI81581	Adi81581 Mouse van
32	1529.4	61.9	2271	12 ADI81615	Adi81615 Mouse glo
33	1522.4	61.7	2736	2 AAX87478	Aax87478 Rat vanil
34	1522.4	61.7	2736	2 AAX19730	Aax19730 Rat VRRP-
35	1507.4	61.1	3025	9 AAL62522	Aal62522 Human tra
36	1459.6	59.1	2286	12 ADI81575	Adi81575 Rat vanil
37	1458	59.1	2286	12 ADI81563	Adi81563 Rat stret
38	1445.6	58.6	2289	12 ADI81627	Adi81627 Rat ion c
39	1224.2	49.6	2126	4 AAH14849	Aah14849 Human cdn
40	1098.4	44.5	1794	3 AAA30256	Aaa30256 Rat parti
41	1007.4	40.8	1489	3 AAA30255	Aaa30255 Human VR-
42	750.8	30.4	884	2 AAX87501	Aax87501 Human van
43	750.8	30.4	884	2 AAX19741	Aax19741 Human VRR
44	750.4	30.4	885	2 AAZ07115	Aaz07115 Human van
45	711	28.8	876	2 AAV59808	Aav59808 Human sec

ALIGNMENTS

RESULT 1
AAC60297
ID AAC60297 standard; DNA; 2469 BP.
XX
AC AAC60297;
XX
DT 14-FEB-2001 (first entry)
XX
DE Human vanilloid receptor like receptor DNA.
XX
KW VR-L; vanilloid receptor-like receptor; pain; infection; allergy;
KW mechanical injury; lymphoid tissue; human; ds.
XX
OS Homo sapiens.
XX
PN GB2346882-A.
XX
PD 23-AUG-2000.
XX
PF 02-DEC-1999; 99GB-00028566.
XX
PR 08-DEC-1998; 98GB-00027016.
XX
(MERI) MERCK SHARP & DOHME LTD.
XX
Bonnert TP;
XX
WFI; 2001-064250/08.
DR P-PSDB; AAB35622.
PT New polynucleotide encoding human vanilloid receptor-like receptor for
PT diagnosing and treating pain, infections, allergies, and cancers.
XX
PS Claim 2; Fig 1; 36pp; English.
XX
CC The present invention relates to the human vanilloid receptor-like
CC receptor. This receptor may be used for diagnosing or treating conditions
CC associated with altered vanilloid receptor-like (VR-L) receptor
CC expression. It may also be used to treat abnormal conditions associated
CC with pain. Conditions or diseases that can be diagnosed or treated
CC include viral, bacterial and fungal infections, allergic responses,
CC mechanical injury associated with trauma, hereditary diseases, lymphoma
CC or carcinoma, or other conditions which activate the genes of the

Db	2041	GTCAACAGTGTGCCACTGACACCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCTGTC	2100
Qy	2101	CTCGAGATGAGAAATGGCTATTGCTGTGCAGGAAGAAGCAGCGGGCAGGTGTGATGCTG	2160
Db	2101	CTCGAGATGAGAAATGGCTATTGCTGTGCAGGAAGAAGCAGCGGGCAGGTGTGATGCTG	2160
Qy	2161	ACCGTTGGCACTAAGCCAGATGGCAGCCCGATGAGCGCTGGTGTCTTCAGGCTGGAGGAG	2220
Db	2161	ACCGTTGGCACTAAGCCAGATGGCAGCCCGATGAGCGCTGGTGTCTTCAGGCTGGAGGAG	2220
Qy	2221	GTCAACTGGGCTTCATGGGAGCAGACGCTGCCCTACGCTGTGTGAGGACCCGTCAGGGGCA	2280
Db	2221	GTGAACTGGGCTTCATGGGAGCAGACGCTGCCCTACGCTGTGTGAGGACCCGTCAGGGGCA	2280
Qy	2281	GGTGTCCCTCGAACTCTCGAGAACCCCTGTCTCGCTTCCCTCCCAAGGAGGATGAGGAT	2340
Db	2281	GGTGTCCCTCGAACTCTCGAGAACCCCTGTCTCGCTTCCCTCCCAAGGAGGATGAGGAT	2340
Qy	2341	GGTGCCTCTCAGGAAAATATGTGCCCGTCCAGCTCTCCAGTCCAACTGATGGCCGAGA	2400
Db	2341	GGTGCCTCTCAGGAAAATATGTGCCCGTCCAGCTCTCCAGTCCAACTGATGGCCGAGA	2400
Qy	2401	TGCAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCCAAACCACTCTCTGCTCTGG	2460
Db	2401	TGCAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCCAAACCACTCTCTGCTCTGG	2460
Qy	2461	GGTCCCACTG	2469
Db	2461	GGTCCCACTG	2469

RESULT 2	
ADP66662	ADP66662 standard; DNA; 2469 BP.
XX	ADP66662;
XX	
XX	ADP66662;
XX	
DT	26-AUG-2004 (first entry)
XX	
DE	Human vanilloid 2 receptor (VR2) polypeptide encoding DNA, SEQ ID 1.
XX	
XX	VR2; vanilloid 2 receptor; tranquilizer; antidepressant; hypnotic; CNS;
KW	toxicolytic; vasotropic; hypotensive; cardiovascular; gynaecological;
KW	analgesic; neuroleptic; anticoagulant; gene therapy; human; gene; ds.
XX	
XX	
OS	Homo sapiens.
XX	
XX	
FH	Key
CDS	Location/Qualifiers
FT	97..2391
FT	/*tag= a
FT	/product= "VR2 polypeptide"
FT	
XX	
XX	WO2004045638-A1.
PN	
XX	
PD	03-JUN-2004.
XX	
PF	18-NOV-2003; 2003WO-GB004988.
XX	
PR	18-NOV-2002; 2002GB-00026850.
PR	18-NOV-2002; 2002GB-00026865.
PR	01-OCT-2003; 2003GB-00022990.
XX	
PA	(MERI) MERCK SHARP & DOHME LTD.
XX	
PI	Oliver KR, Seabrook GR, Wainwright A;
XX	
DR	WPI; 2004-431843/40.
DR	P-PSDB; ADP66663.
XX	
PT	Use of vanilloid receptor-2 ligands for treating and/or preventing
PT	anxiety, depression, circadian rhythm disorders, pre-term labor, erectile
PT	dysfunction, hypertension, eclampsia and/or schizophrenia.
XX	
XX	

PS Claim 22; Fig 1; 46pp; English.

XX

The invention relates to a compound selected from a vanilloid 2 receptor (VR2) polypeptide, a compound which modulates the activity of a VR2 polypeptide, a polynucleotide encoding a VR2 polypeptide, or an antisense polynucleotide. The compound is used for the manufacture of a medicament for treating anxiety, depression, circadian rhythm disorders, pre-term labour, erectile dysfunction, hypertension and/or eclampsia and associated disorders, and/or schizophrenia. The compound may also be used for inducing diuresis and/or inhibiting platelet aggregation. The compound may also be used for manufacturing a medicament for treating the disorders mentioned above. The medicament enhances or improves sleep quality and/or is used for preventing and/or treating sleep disorders and sleep disturbances by increasing sleep efficiency and augmenting sleep maintenance in a mammal, or for achieving a circadian rhythm phase-shifting effect, for resetting the internal circadian clock or for shortening the time of reentrainment of circadian rhythms in a mammal. The present sequence represents a DNA encoding a human VR2 polypeptide.

CC

XX

SQ Sequence 2469 BP; 510 A; 724 C; 710 G; 525 T; 0 U; 0 Other;

Query Match	100.0%;	Score	2469;	DB	12;	Length	2469;
Best Local Similarity	100.0%;	Pred. No. 0;					
Matches 2469;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
Qy	1	CACGAGGCCACGGCAGCTGGGAGGAGACAGGACCCTTGACATCTCCATCTGCACAGA	60				
Db	1	CACGAGGCCACGGCAGCTGGGAGGAAAGACAGGACCCTTGACATCTCCATCTGCACAGA	60				
Qy	61	GGTCCTGGCTGGACCGAGCACGCTCTCTCTCTTAGGATGACTTCAACCTCCAGCTCTTCCA	120				
Db	61	GGTCCTGGCTGGACCGAGCACGCTCTCTCTCTTAGGATGACTTCAACCTCCAGCTCTTCCA	120				
Qy	121	GTTTTTCAGGTTGGAGACATTAGATFGAGGCCAAGAAGATGGCTCTGAGGCGGACAGAGGA	180				
Db	121	GTTTTTCAGGTTGGAGACATTAGATFGAGGGCCCAAGAAGATGGCTCTGAGGCGGACAGAGGA	180				
Qy	181	AAGCTGGAATTTGGGAGGGGGCTGCCTCCCATGAGTGCACATGTTCCAGGGGGAGGACCGG	240				
Db	181	AAGCTGGAATTTGGGAGGGGGCTGCCTCCCATGAGTGCACATGTTCCAGGGGGAGGACCGG	240				
Qy	241	AAATTCGCCCTCAGATAAAGAGTCAACCTCAACTACCGAAAGGAAACAGGTGCCAGTCAG	300				
Db	241	AAATTCGCCCTCAGATAAAGAGTCAACCTCAACTACCGAAAGGAAACAGGTGCCAGTCAG	300				
Qy	301	CCGGATCCAAACCGATTTGACCGAGATCGGCTCTTCAATGGGTCTCTCCGGGGTGTCCCC	360				
Db	301	CCGGATCCAAACCGATTTGACCGAGATCGGCTCTTCAATGGGTCTCTCCGGGGTGTCCCC	360				
Qy	361	GAGGATCTGGCTGGACTTCCAGAGTACTGAGCAAGACCAACAAGTACTTCAACGACTCG	420				
Db	361	GAGGATCTGGCTGGACTTCCAGAGTACTGAGCAAGACCAACAAGTACTTCAACGACTCG	420				
Qy	421	GAATACACAGAGGGCTCCACAGGTAAAGACGTGCCTGATGAAAGGCTGTGTCAAACCTTAAG	480				
Db	421	GAATACACAGAGGGCTCCACAGGTAAAGACGTGCCTGATGAAAGGCTGTGTCAAACCTTAAG	480				
Qy	481	GACGGAGTCAATGCTGTGAATTTCTGCCACTGTCTGCAGATCGACAGGGAATCTTGGCAATCCT	540				
Db	481	GACGGAGTCAATGCTGTGAATTTCTGCCACTGTCTGCAGATCGACAGGGAATCTTGGCAATCCT	540				
Qy	541	CAGCCCCTGGTAATATGCCAGTGCACAGATCACTATTACCGAGGCCACAGCGCTCTGCAC	600				
Db	541	CAGCCCCTGGTAATATGCCAGTGCACAGATCACTATTACCGAGGCCACAGCGCTCTGCAC	600				
Qy	601	ATCGCCATTGGAAGAAGAGAGTCTTCGAGTGTGTGAAGCTCTTGGTGGAGAAATGGGGCCAAAT	660				
Db	601	ATCGCCATTGGAAGAAGAGAGTCTTCGAGTGTGTGAAGCTCTTGGTGGAGAAATGGGGCCAAAT	660				
Qy	661	GTGANATGCCGGGCTCGGGCGGCTCTTTCAGAAAGGGCCAAAGGACTTGTCTTTATTTC	720				
Db	661	GTGANATGCCGGGCTCGGGCGGCTCTTTCAGAAAGGGCCAAAGGACTTGTCTTTTATTTC	720				

QY 721 GGTGAGTACCCCTCTCTTTGGCCGCTTGACCAAGCAGTGGATGTGTTAGCTTACCTC 780
 Db 721 GGTGAGTACCCCTCTCTTTGGCCGCTTGACCAAGCAGTGGATGTGTTAGCTTACCTC 780
 QY 781 CTGGAGAAACCAACACAGAGCCCGCAGCTTGACAGCCACTGACTCCAGGCGCAACAGATC 840
 Db 781 CTGGAGAAACCAACACAGAGCCCGCAGCTTGACAGCCACTGACTCCAGGCGCAACAGATC 840
 QY 841 CTGCATGCCCTAGTATGATCTCGGACAACTCAGCTGAGAAATGCACTGTGTGACACAGC 900
 Db 841 CTGCATGCCCTAGTATGATCTCGGACAACTCAGCTGAGAAATGCACTGTGTGACACAGC 900
 QY 901 ATGTATGATGGGCTCTCAAGCTGGGGCCCGCTCTGCGCTTACCGTGCAGCTTGAGGAC 960
 Db 901 ATGTATGATGGGCTCTCAAGCTGGGGCCCGCTCTGCGCTTACCGTGCAGCTTGAGGAC 960
 QY 961 ATCCGCAACTGCAGGATCTCAGCCCTCTGAAGCTGGCCGCGCAAGAGGCGCAAGATCGAG 1020
 Db 961 ATCCGCAACTGCAGGATCTCAGCCCTCTGAAGCTGGCCGCGCAAGAGGCGCAAGATCGAG 1020
 QY 1021 ATTTTCAGGCACATCTGCGAGCGGAGTTTTCAGGACTGAGCCACTTTCCCGAAAGTTTC 1080
 Db 1021 ATTTTCAGGCACATCTGCGAGCGGAGTTTTCAGGACTGAGCCACTTTCCCGAAAGTTTC 1080
 QY 1081 ACCGAGTGTGCTATGGGCTGTCCGGGTGTGCTGTATGACCTGGCTTCTGTGGACAGC 1140
 Db 1081 ACCGAGTGTGCTATGGGCTGTCCGGGTGTGCTGTATGACCTGGCTTCTGTGGACAGC 1140
 QY 1141 TGTGAGGAGAACTCAGTGTGAGATCATTTGCCCTTTTCATTGCAAGAGCCCGCACCGACAC 1200
 Db 1141 TGTGAGGAGAACTCAGTGTGAGATCATTTGCCCTTTTCATTGCAAGAGCCCGCACCGACAC 1200
 QY 1201 CGAATGGTGTGTTGAGGCCCTTGAAACAACTCTGCGAGCGGAAATGGGATCTGCTCATC 1260
 Db 1201 CGAATGGTGTGTTGAGGCCCTTGAAACAACTCTGCGAGCGGAAATGGGATCTGCTCATC 1260
 QY 1261 CCCAAGTTCTTAACTTCCTGTGTAATCTGATCTACATGTTTCAATCTTCAACCGCTGT 1320
 Db 1261 CCCAAGTTCTTAACTTCCTGTGTAATCTGATCTACATGTTTCAATCTTCAACCGCTGT 1320
 QY 1321 GCCTACCATCAGCTTACCTTGAAAGAGAGCGCCCGCTTCACTGAAAGCGAGGTTGGA 1380
 Db 1321 GCCTACCATCAGCTTACCTTGAAAGAGAGCGCCCGCTTCACTGAAAGCGAGGTTGGA 1380
 QY 1381 AACTCCATGTCTGAGCGGCCACATCTTATCTGCTAGGGGGATCTACCTCTCTCGTG 1440
 Db 1381 AACTCCATGTCTGAGCGGCCACATCTTATCTGCTAGGGGGATCTACCTCTCTCGTG 1440
 QY 1441 GGCAGCTGTGTACTTCTGGCGGCCAGCTGTTCTATCTGGATCTCGTTTCATAGACAGC 1500
 Db 1441 GGCAGCTGTGTGTACTTCTGGCGGCCAGCTGTTCTATCTGGATCTCGTTTCATAGACAGC 1500
 QY 1501 TACTTTGAAATCTCTTCTGTTTCCAGGCCCTGCTCACAGTGTGTGCCAGGTGCTGTGT 1560
 Db 1501 TACTTTGAAATCTCTTCTGTTTCCAGGCCCTGCTCACAGTGTGTGCCAGGTGCTGTGT 1560
 QY 1561 TTCTGGCCATCAGTGTGTTACCTGCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 Db 1561 TTCTGGCCATCAGTGTGTTACCTGCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 QY 1621 AACTGCTTTACTATACAGTGGCTTCCAGCACAGGCACTACAGTGTCTATGATCCAG 1680
 Db 1621 AACTGCTTTACTATACAGTGGCTTCCAGCACAGGCACTACAGTGTCTATGATCCAG 1680
 QY 1681 AAGTCACTCTGGGACCTGCTGCTGCTTCTGATCTTACTTACTTCTTCTTCTTCTGGC 1740
 Db 1681 AAGTCACTCTGGGACCTGCTGCTGCTTCTGATCTTACTTACTTCTTCTTCTTCTGGC 1740
 QY 1741 TTCTGCTGTAGCCCTGTGTGAGCTGAGCCAGGAGGCTTGGCGCCCGGAGCTCTACAGGC 1800
 Db 1741 TTCTGCTGTAGCCCTGTGTGAGCTGAGCCAGGAGGCTTGGCGCCCGGAGCTCTACAGGC 1800
 QY 1801 CCCAATGCCACAGTCTAGTGACCCATCGAGGGGACAGGAGGACGAGGGCAACGGGGCC 1860

Db 1801 CCCAATGCCACAGTCTAGTGACCCATGAGGGACAGGAGGACGAGGGCAACGGGGCC 1860
 QY 1861 CAGTACAGGGGTATCTCGAAGCCTCTTGGAGCTCTTCAAATTCACCATCGGCATGGGC 1920
 Db 1861 CAGTACAGGGGTATCTCGAAGCCTCTTGGAGCTCTTCAAATTCACCATCGGCATGGGC 1920
 QY 1921 GAGCTGGCTTCCAGAGCAGTGCACCTTCCGGGCATGGTCTGCTGCTGCTGCTG 1980
 Db 1921 GAGCTGGCTTCCAGAGCAGTGCACCTTCCGGGCATGGTCTGCTGCTGCTGCTG 1980
 QY 1981 TACGTGCTGCTCACCTACATCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACC 2040
 Db 1981 TACGTGCTGCTCACCTACATCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACC 2040
 QY 2041 GTCAAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTC 2100
 Db 2041 GTCAAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTC 2100
 QY 2101 CTGGAGATGGAGAAATGGCTATTGGTGTGCGAGGAAGCAGCGGCGAGGTGTGATGCTG 2160
 Db 2101 CTGGAGATGGAGAAATGGCTATTGGTGTGCGAGGAAGCAGCGGCGAGGTGTGATGCTG 2160
 QY 2161 ACCGTTGGCACTTAAGCCAGATGGCAGCCCGATGAGCGCTGCTTCAAGGCTGGAGGAG 2220
 Db 2161 ACCGTTGGCACTTAAGCCAGATGGCAGCCCGATGAGCGCTGCTTCAAGGCTGGAGGAG 2220
 QY 2221 GTGAACTGGGCTTCAATGGAGCAGACGCTGCTCA CGCTGTGTGAGGACCCGTCAGGGCA 2280
 Db 2221 GTGAACTGGGCTTCAATGGAGCAGACGCTGCTCA CGCTGTGTGAGGACCCGTCAGGGCA 2280
 QY 2281 GGTGTCCCTCGAATCTCGAGAACCTTCTGAGAACCTTCTGCTGGCTTCCCAAGAGGATGAGGAT 2340
 Db 2281 GGTGTCCCTCGAATCTCGAGAACCTTCTGAGAACCTTCTGCTGGCTTCCCAAGAGGATGAGGAT 2340
 QY 2341 GGTGCTCTGAGGAAATATATGTGCCCTGCAAGCTCTCCAGTCCCACTGATGGCCACAG 2400
 Db 2341 GGTGCTCTGAGGAAATATATGTGCCCTGCAAGCTCTCCAGTCCCACTGATGGCCACAG 2400
 QY 2401 TGCAGAGGAGGCCACAGAGACAGAGAGAGATCTTTCCACCAACATCTGCTGGCTCTGG 2460
 Db 2401 TGCAGAGGAGGCCACAGAGACAGAGAGAGATCTTTCCACCAACATCTGCTGGCTCTGG 2460
 QY 2461 GGTGCCAGT 2469
 Db 2461 GGTGCCAGT 2469

RESULT 3

AAA30254
 ID AAA30254 standard; cDNA; 2809 BP.
 XX
 AC AAA30254;
 XX
 DT 05-SEP-2000 (first entry)
 XX
 DE Human VR-2 coding sequence.
 XX
 KW VR-2; human; vanilloid receptor; nociceptor; pain signalling;
 KW hyperalgesia; musculoskeletal disorder; neuropathic pain;
 KW chromosome 17p11-12; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 361..2655
 FT /*tag= a
 FT /product= "VR-2"
 FT /note= "This region is specifically claimed"
 XX
 PN WO200029577-A1.
 XX
 PD 25-MAY-2000.

Qy	183	GCTGGATTTTGGAGCGGGCTGCTCCATGGAGTCACAGTTCCAGGGGAGGACCGGAA	242	Qy	1263	CAAGTTCTTTAAATCTTCTGTGTAATCTGATCTACATGTTCACTTCAACGCTGTTC	1322
Db	447	GCTGGATTTTGGAGCGGGCTGCTCCATGGAGTCACAGTTCCAGGGGAGGACCGGAA	506	Db	1527	CAAGTTCTTTAAATCTTCTGTGTAATCTGATCTACATGTTCACTTCAACGCTGTTC	1586
Qy	243	ATTGCGCCCTCAGATAAGAGTCAACCTCACTACCGAAAGGGAAACAGGTGCCAGTCAGCC	302	Qy	1323	CTACCATCAGCCTACCTGAAAGACGAGCGCCCTCACCTCAGCTGAAGACGAGGTTGGAAA	1382
Db	507	ATTGCGCCCTCAGATAAGAGTCAACCTCACTACCGAAAGGGAAACAGGTGCCAGTCAGCC	566	Db	1587	CTACCATCAGCCTACCTGAAAGACGAGCGCCCTCACCTCAGCTGAAGACGAGGTTGGAAA	1646
Qy	303	GGATCCMAACCGATTGGAACGAGATGGCTCTTCAATGGGTCTCCGGGGTGTCCCCGA	362	Qy	1383	CTCCATGCTGCTGACGCGGCCACATCTTATCTCTGTAGGGGGGATCTACCTCTCGTGGG	1442
Db	567	GGATCCMAACCGATTGGAACGAGATGGGTCTTCAATGGGTCTCCGGGGTGTCCCCGA	626	Db	1647	CTCCATGCTGCTGACGCGGCCACATCTTATCTCTGTAGGGGGGATCTACCTCTCGTGGG	1706
Qy	363	GGATCTGGCTGGATTTCCACAGTACCTTGACCAAGACCAGCAAGTACTCACCGACTCGGA	422	Qy	1443	CCAGCTGTGCTTCTTCCAGCGCCCTGCTCAGAGTGTGTCCAGAGCTGCTGTTT	1502
Db	627	GGATCTGGCTGGATTTCCACAGTACCTTGACCAAGACCAGCAAGTACTCACCGACTCGGA	686	Db	1707	CCAGCTGTGCTTCTTCCAGCGCCCTGCTCAGAGTGTGTCCAGAGCTGCTGTTT	1766
Qy	423	ATACACAGAGGGCTCCACAGTAAGAGTGCCTCTGATGAAGGCTGTGCTGAACCTTAAGGA	482	Qy	1503	CTTTGAAATCCTTCTTCTGTTCCAGGCCCTGCTCAGAGTGTGTCCAGAGCTGCTGTTT	1562
Db	687	ATACACAGAGGGCTCCACAGTAAGAGTGCCTCTGATGAAGGCTGTGCTGAACCTTAAGGA	746	Db	1767	CTTTGAAATCCTTCTTCTGTTCCAGGCCCTGCTCAGAGTGTGTCCAGAGCTGCTGTTT	1826
Qy	483	CGAGTCAATGCTGCTGCAATCTGCGCACTGCTGCAAGTCGACAGGACTCTGGCAATCTCA	542	Qy	1563	CTTGGCCATCGAGTGTGACTGCTGCTGCTGTGTCTGCGCTGCTGCTGGCTGGCTGAA	1622
Db	747	CGAGTCAATGCTGCTGCAATCTGCGCACTGCTGCAAGTCGACAGGACTCTGGCAATCTCA	806	Db	1827	CTTGGCCATCGAGTGTGACTGCTGCTGCTGTGTCTGCGCTGCTGCTGGCTGGCTGAA	1886
Qy	543	GCCCTCGTAAATGCCAGTGCAAGATGACTATTACCGAGGCCACAGGCTCTGCGACAT	602	Qy	1623	CCTGCTTTACTATACACGTGGCTTCCAGCACAGGCACTACAGTGTCTATGATCCAGAA	1682
Db	807	GCCCTCGTAAATGCCAGTGCAAGATGACTATTACCGAGGCCACAGGCTCTGCGACAT	866	Db	1887	CCTGCTTTACTATACACGTGGCTTCCAGCACAGGCACTACAGTGTCTATGATCCAGAA	1946
Qy	603	CGCATTTGAGAAGAGGAGTCTGACAGTGTGTGAAGCTCTGCTGGAGAAATGGGGCCAAATGT	662	Qy	1683	GGTCATCTCGGGGACTGCTGGGCTTCTTCTGATCTACTTACTTCTTCTTCTTCTTCTT	1742
Db	867	CGCATTTGAGAAGAGGAGTCTGACAGTGTGTGAAGCTCTGCTGGAGAAATGGGGCCAAATGT	926	Db	1947	GGTCATCTCGGGGACTGCTGGGCTTCTTCTGATCTACTTACTTCTTCTTCTTCTTCTT	2006
Qy	663	GCATGCCCGGGCTGCGGGCGCTTCTTCCAGAGGGCCAAAGGGACTTTGCTTTTATTTCGG	722	Qy	1743	CGCTGTAGCCCTGTGTCAGCTGAGCCAGGAGGCTTGGCGCCCGGAAAGCTCTTACAGGCC	1802
Db	927	GCATGCCCGGGCTGCGGGCGCTTCTTCCAGAGGGCCAAAGGGACTTTGCTTTTATTTCGG	986	Db	2007	CGCTGTAGCCCTGTGTCAGCTGAGCCAGGAGGCTTGGCGCCCGGAAAGCTCTTACAGGCC	2066
Qy	723	TGAGCTACCCCTCTCTTTGGCGCTTCCACACAGCTGGAGTGTGTAAGCTACCTCT	782	Qy	1803	CAATGCCACAGAGTCACTGTCAGCCATGAGGAGGACAGGAGGACAGGGGCGGCGCA	1862
Db	987	TGAGCTACCCCTCTCTTTGGCGCTTCCACACAGCTGGAGTGTGTAAGCTACCTCT	1046	Db	2067	CAATGCCACAGAGTCACTGTCAGCCATGAGGAGGACAGGAGGACAGGGGCGGCGCA	2126
Qy	783	GGAGAACCCACACAGCCCGCCAGCTGCGAGGCCACTGACTCCCGAGGGCAACACAGTCT	842	Qy	1863	GTAACGGGTATCCTTGGAGCTCCTTGGAGCTTCTTCAATTCACCATCGGCAATGGGCGA	1922
Db	1047	GGAGAACCCACACAGCCCGCCAGCTGCGAGGCCACTGACTCCCGAGGGCAACACAGTCT	1106	Db	2127	GTAACGGGTATCCTTGGAGCTCCTTGGAGCTTCTTCAATTCACCATCGGCAATGGGCGA	2186
Qy	843	GCATGCCCTAGTATGATCTCGGACAACTCAGCTGAGAAATTTGCACTGTGTGACAGCAT	902	Qy	1923	GCTGGCTTCCAGGACAGCTGCATTTCCGCGCATGGTGTCTGCTGCTGCTGGCTGCTA	1982
Db	1107	GCATGCCCTAGTATGATCTCGGACAACTCAGCTGAGAAATTTGCACTGTGTGACAGCAT	1166	Db	2187	GCTGGCTTCCAGGACAGCTGCATTTCCGCGCATGGTGTCTGCTGCTGCTGGCTGCTA	2246
Qy	903	GTATGATGGGCTCTCCAGCTGGGGCCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	962	Qy	1983	CGTGTGCTCACCTACATCCTGCTGCTCAAATGCTCATCGCTCATGAGCGAGACCGT	2042
Db	1167	GTATGATGGGCTCTCCAGCTGGGGCCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1226	Db	2247	CGTGTGCTCACCTACATCCTGCTGCTCAAATGCTCATCGCTCATGAGCGAGACCGT	2306
Qy	963	CCGCAACTGACAGATCTCACGCTCTGAAAGCTGGCGCCCAAGGAGGGCAAGATCCGAGAT	1022	Qy	2043	CAAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGCGAAGGCACTCTGTCTCT	2102
Db	1227	CCGCAACTGACAGATCTCACGCTCTGAAAGCTGGCGCCCAAGGAGGGCAAGATCCGAGAT	1286	Db	2307	CAAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGCGAAGGCACTCTGTCTCT	2366
Qy	1023	TTTCAGGCACATCTGACAGCGGAGTTTTCAGGACTGAGGCACTGAGGCACTTTTCCGAAAGTTTCA	1082	Qy	2103	GGAGATGGAGATGGCTATTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2162
Db	1287	TTTCAGGCACATCTGACAGCGGAGTTTTCAGGACTGAGGCACTGAGGCACTTTTCCGAAAGTTTCA	1346	Db	2367	GGAGATGGAGATGGCTATTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2426
Qy	1083	CGAGTGTGCTATGGGCTGTCCGGGTGTGCTGTATGACTGCTGCTGCTGCTGCTGCTGCTG	1142	Qy	2163	CGTGTGGCACTAAGCCAGATGGCAGCGCTGAGCGCTGCTGCTTCAAGGTTGAGGAGGAGT	2222
Db	1347	CGAGTGTGCTATGGGCTGTCCGGGTGTGCTGTATGACTGCTGCTGCTGCTGCTGCTGCTG	1406	Db	2427	CGTGTGGCACTAAGCCAGATGGCAGCGCTGAGCGCTGCTGCTTCAAGGTTGAGGAGGAGT	2486
Qy	1143	TGAGAGAACTCAGTGTGAGATCATTTGCTCTTTCATTTGCAAGAGCCCGACACGACCG	1202	Qy	2223	GAACTGGCTTTCATGGAGCAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2282
Db	1407	TGAGAGAACTCAGTGTGAGATCATTTGCTCTTTCATTTGCAAGAGCCCGACACGACCG	1466	Db	2487	GAACTGGCTTTCATGGAGCAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2546
Qy	1203	AATGGTCTTTTGGAGCCCTTGAAACAACTGCTGAGCGGAAATGGGATCTGCTCATCCC	1262	Qy	2283	TGTCCTCTCGAACTCTCGAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2342
Db	1467	AATGGTCTTTTGGAGCCCTTGAAACAACTGCTGAGCGGAAATGGGATCTGCTCATCCC	1526	Db	2547	TGTCCTCTCGAACTCTCGAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2606
				Qy	2343	TGCTCTGAGGAAAACTATGCTGCCGCTCCAGCTCTCCAGTCCAACTGATGGGCCCAAGT	2402

Db 2607 TGGCTCTGAGGAAATATGTGCGCTCCAGCTCCAGTCCAGTCCAGTATGAGCCAGATG 2666
QY 2403 CAGCAGAGGCCAGAGGACAGAGCAGAGGATCTTTCCAAACCAATCTGCTGGCTTGGGG 2462
Db 2667 CAGCAGAGGCCAGAGGACAGAGCAGAGGATCTTTCCAAACCAATCTGCTGGCTTGGGG 2726
QY 2463 TCCCACT 2469
Db 2727 TCCCACT 2733

RESULT 5
ADQ83962
ID ADQ83962 standard; cDNA; 2774 BP.
XX AC ADQ83962;
XX DT 07-OCT-2004 (first entry)
XX Human tumour-associated antigenic target (TAT) cDNA sequence #776.
XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
XX cancer; cell proliferative disorder; gene; ss.
XX Homo sapiens.
XX WO2004060270-A2.
XX 22-JUL-2004.
XX 15-OCT-2003; 2003WO-US029126.
XX 18-OCT-2002; 2002US-0418988P.
XX (GETH) GENENTECH INC.
XX (WUTD/) WU T D.
XX (ZHOU/) ZHOU Y.
XX Wu TD, Zhou Y;
XX WPI; 2004-534300/51.
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
XX preventing or treating cell proliferative disorders such as cancer.
XX Claim 1; SEQ ID NO 776; 5504pp; English.

The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising

CC cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

XX Sequence 2774 BP; 560 A; 827 C; 799 G; 588 T; 0 U; 0 Other;
SQ
Query Match 99.7%; Score 2460.6; DB 13; Length 2774;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2463; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 CGAGCCGACGCGCAGCTGGGAGGAGACAGACCCCTTGACATCTCCATCTGCACAGAG 62
Db 274 CAACACCGACGCGCAGCTGGGAGGAGACAGACCCCTTGACATCTCCATCTGCACAGAG 333
QY 63 TCCTGGCTGGACCGAGCAGCCTCCCTCCTAGGATGACCTCACCCCTCCAGCTCTCCAGT 122
Db 334 TCCTGGCTGGACCGAGCAGCCTCCCTCCTAGGATGACCTCACCCCTCCAGCTCTCCAGT 393
QY 123 TTTCAAGTTGGAGACATTAGATGGAGGCGCAAGAGATGGCTCTGAGGCGGACAGAGGAAA 182
Db 394 TTTCAAGTTGGAGACATTAGATGGAGGCGCAAGAGATGGCTCTGAGGCGGACAGAGGAAA 453
QY 183 GCTGATTTTGGAGGGGGCTGCCCTCCATGAGTCACTTCCAGGGGAGGACCGGAA 242
Db 454 GCTGATTTTGGAGGGGGCTGCCCTCCATGAGTCACTTCCAGGGGAGGACCGGAA 513
QY 243 ATTTGCCCTCAGATAAGAGTCAACCTCAACTACCGAAAGGAAACAGGTGCCAGTCAGCC 302
Db 514 ATTTGCCCTCAGATAAGAGTCAACCTCAACTACCGAAAGGAAACAGGTGCCAGTCAGCC 573
QY 303 GGATCCAAACCGATTGTGACCGAGATGGGCTCTTCAATCGGCTCTCCCGGGGTGTCGCCGA 362
Db 574 GGATCCAAACCGATTGTGACCGAGATCGGCTCTTCAATCGGCTCTCCCGGGGTGTCGCCGA 633
QY 363 GGATCTGGCTGACATCTCCAGAGTACTTGAGCAGAGACCCAGCAGTACTCACCGACTCGGA 422
Db 634 GGATCTGGCTGACATCTCCAGAGTACTTGAGCAGAGACCCAGCAGTACTCACCGACTCGGA 693
QY 423 ATACACAGAGGGCTCCACAGGTAAAGACGTGCCTGTGATGAAGGGTGTGCTGAAACCTTAAGGA 482
Db 694 ATACACAGAGGGCTCCACAGGTAAAGACGTGCCTGTGATGAAGGGTGTGCTGAAACCTTAAGGA 753
QY 483 CGGAGTCAATGGCTGCATTCTGCCACTGTGCAGATCGACAGGGAATCTTGGCAATCCTCA 542
Db 754 CGGAGTCAATGGCTGCATTCTGCCACTGTGCAGATCGACAGGGAATCTTGGCAATCCTCA 813
QY 543 GCCCTGTGTAATGCCACGTGACAGATCACTATTACCGAGGCCACAGGCTCTGCACAT 602
Db 814 GCCCTGTGTAATGCCACGTGACAGATCACTATTACCGAGGCCACAGGCTCTGCACAT 873
QY 603 CGCCATTGAGAGAGAGGTCTGCAGTGTGTGAAGCTCTCTGTGGAGAAATGGGGCCCAATGT 662
Db 874 CGCCATTGAGAGAGAGGTCTGCAGTGTGTGAAGCTCTCTGTGGAGAAATGGGGCCCAATGT 933
QY 663 GCATGCCCGGGCTCGGGCGGCTTTTCAGAGGGGCCAAGGGAATTTGCTTTTATTTTCGG 722
Db 934 GCATGCCCGGGCTCGGGCGGCTTTTCAGAGGGGCCAAGGGAATTTGCTTTTATTTTCGG 993
QY 723 TGAGCTACCCCTCTCTTTGGCGGCTTGACACAGCAGTGGGATGTGTTAGCTTACCTCCT 782
Db 994 TGAGCTACCCCTCTCTTTGGCGGCTTGACACAGCAGTGGGATGTGTTAGCTTACCTCCT 1053
QY 783 GGAGAAACCCACACAGCCCGGCCAGCTGCAGGGCCACTGACTCCCGAGGGCAACACAGTCTCT 842

DR WPI; 2004-419628/39.
DR P-PSDB; ADP25061.
XX
PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
PS Claim 1; SEQ ID NO 2238; 2940pp; English.
XX
CC The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polynuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence encodes a PRO protein of
CC the invention.
XX
SQ Sequence 2807 BP; 586 A; 829 C; 804 G; 588 T; 0 U; 0 Other;
Query Match 99.7%; Score 2460,6; DB 13; Length 2807;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2463; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 CGAGGGCGACGCGCAGCTGGGAGGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG 62
DB |||||
QY 283 CAACACCGACGCGCAGCTGGGAGGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG 342
DB |||||
QY 63 TCCTGGCTGGACCGAGCAGCTCTCTCTAGATGACCTCACCTCCAGCTCTCCAGT 122
DB |||||
QY 343 TCCTGGCTGGACCGAGCAGCTCTCTCTAGATGACCTCACCTCCAGCTCTCCAGT 402
DB |||||
QY 123 TTTTCAGGCTCGAGACATTTAGATGAGGCGCAAGAGATGGCTCTGAGCGGACAGAGGAAA 182
DB |||||
QY 403 TTTTCAGGCTCGAGACATTTAGATGAGGCGCAAGAGATGGCTCTGAGCGGACAGAGGAAA 462
DB |||||
QY 183 GCTGGATTTTGGAGCGGGCTGCCCTCCATGGAGTCAAGTTCAGGGCGAGGACCGGAA 242
DB |||||
QY 463 GCTGGATTTTGGAGCGGGCTGCCCTCCATGGAGTCAAGTTCAGGGCGAGGACCGGAA 522
DB |||||
QY 243 ATTGCGCCCTCAGATAAGATCAACCTCAACTACCGAAGGGAACAGGTGCCAGTCAGCC 302
DB |||||
QY 523 ATTGCGCCCTCAGATAAGATCAACCTCAACTACCGAAGGGAACAGGTGCCAGTCAGCC 582
DB |||||
QY 303 GGAATCCAAACCGATTTTTCAGCGAGATCGGCTCTTCAATCGCGGTCTCCCGGGGTGTCGCCGA 362
DB |||||
QY 583 GGAATCCAAACCGATTTTTCAGCGAGATCGGCTCTTCAATCGCGGTCTCCCGGGGTGTCGCCGA 642
DB |||||
QY 363 GGATCTGGCTGGACTTCACAGATGATCTGAGCAAGACCAAGTACCTCACCGACTCGGA 422
DB |||||
QY 643 GGATCTGGCTGGACTTCACAGATGATCTGAGCAAGACCAAGTACCTCACCGACTCGGA 702
DB |||||
QY 423 ATACACAGAGGGCTCCACAGGTAGACGTGCCTGATGAAGGCTGTGCTGAACCTTAAGGA 482
DB |||||

DB |||||
703 ATACACAGAGGGCTCCACAGGTAAAGCTGCTGATGAAGGCTGTGCTGAACCTTAAGGA 762
QY |||||
483 CGGAGTCAATGCTCGCATTTCTGCCCATCTGCTGCAGATCGACAGGACTCTGGCAATCTCTCA 542
DB |||||
763 CGGAGTCAATGCTCGCATTTCTGCCCATCTGCTGCAGATCGACAGGACTCTGGCAATCTCTCA 822
QY |||||
543 GCCCTCTGTAATGCTCGCATTTCTGCCCATCTGCTGCAGATCGACAGGACTCTGGCAATCTCTCA 602
DB |||||
823 GCCCTCTGTAATGCTCGCATTTCTGCCCATCTGCTGCAGATCGACAGGACTCTGGCAATCTCTCA 882
QY |||||
603 GCCCATTTGAGAAGAGAGTCTGCAGTGTGTGAAGCTCTCTGCTGAGAAATGGGGCCCAATCT 662
DB |||||
883 GCCCATTTGAGAAGAGAGTCTGCAGTGTGTGAAGCTCTCTGCTGAGAAATGGGGCCCAATCT 942
QY |||||
663 GCATGCCCGGGCTCGGGCCGCTCTTCTCCAGAAGGCCCAAGGAGACTTGTCTTTTATTTTCGG 722
DB |||||
943 GCATGCCCGGGCTCGGGCCGCTCTTCTCCAGAAGGCCCAAGGAGACTTGTCTTTTATTTTCGG 1002
QY |||||
723 TGAGCTACCCCTCTCTTTTGGCCGCTTGACCAAGCAGTGGGATGTGTTAAGCTACCTCTCT 782
DB |||||
1003 TGAGCTACCCCTCTCTTTTGGCCGCTTGACCAAGCAGTGGGATGTGTTAAGCTACCTCTCT 1062
QY |||||
783 GGAGAACCCACACACAGCCGCTGTCAGGCCCACTGACTCCAGGGGCAACACAGTCTCT 842
DB |||||
1063 GGAGAACCCACACACAGCCGCTGTCAGGCCCACTGACTCCAGGGGCAACACAGTCTCT 1122
QY |||||
843 GCATGCCCTTAGTGATGATCTCGGACAACTCAGCTGAGAAATTTGACTGGTCAACAGCAT 902
DB |||||
1123 GCATGCCCTTAGTGATGATCTCGGACAACTCAGCTGAGAAATTTGACTGGTCAACAGCAT 1182
QY |||||
903 GTATGATGGGCTCTTCAAGCTGGGGCCGCTCTGCTGCCCTACCGTGACGCTTTGAGGACAT 962
DB |||||
1183 GTATGATGGGCTCTTCAAGCTGGGGCCGCTCTGCTGCCCTACCGTGACGCTTTGAGGACAT 1242
QY |||||
963 CGCAACCTGTCAGGATCTCACGCCCTCTGAAGCTGGCCCGCCCAAGGAGGCAAGATCGAGAT 1022
DB |||||
1243 CGCAACCTGTCAGGATCTCACGCCCTCTGAAGCTGGCCCGCCCAAGGAGGCAAGATCGAGAT 1302
QY |||||
1023 TTTTCAGGCAATCTCTGACGCGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTTCA 1082
DB |||||
1303 TTTTCAGGCAATCTCTGACGCGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTTCA 1362
QY |||||
1083 CGAGTGGTCTATGGGCTGTCCGGGTGTCCGTGTATGACCTGGCTTCTGTGACAGCTG 1142
DB |||||
1363 CGAGTGGTCTATGGGCTGTCCGGGTGTCCGTGTATGACCTGGCTTCTGTGACAGCTG 1422
QY |||||
1143 TGAGGAGAACTCAGTCTCGAGATCAATTCGCTTTTCAATGCAAGAGCCCGCACCGACACCG 1202
DB |||||
1423 TGAGGAGAACTCAGTCTCGAGATCAATTCGCTTTTCAATGCAAGAGCCCGCACCGACACCG 1482
QY |||||
1203 AATGCTGTTTTGGAGCCCTGAAACAACTGCTGACAGGCGAAATGGGATCTGCTCATCCC 1262
DB |||||
1483 AATGCTGTTTTGGAGCCCTGAAACAACTGCTGACAGGCGAAATGGGATCTGCTCATCCC 1542
QY |||||
1263 CAAGTTCTTTTAAACTTCTGTGTAATCTGATCTACATGTTTCATCTTCCAGCTCTGTC 1322
DB |||||
1543 CAAGTTCTTTTAAACTTCTGTGTAATCTGATCTACATGTTTCATCTTCCAGCTCTGTC 1602
QY |||||
1323 CTACCATCAGCTTACCTCTGAAAGAGCAGCCCGCCCTCACCTGAAAGCGGAGGTTTGGAAA 1382
DB |||||
1603 CTACCATCAGCTTACCTCTGAAAGAGCAGCCCGCCCTCACCTGAAAGCGGAGGTTTGGAAA 1662
QY |||||
1383 CTTCATGCTGCTGACGGGCCACATCTTTATTCCTGTAGGGGGATCTACTCTCTCTGTTGG 1442
DB |||||
1663 CTTCATGCTGCTGACGGGCCACATCTTTATTCCTGTAGGGGGATCTACTCTCTCTGTTGG 1722
QY |||||
1443 CGAGCTGTGGTACTTCTGGGGGGCCACGCTGTTTCATCTGATCTCTGTTTCATACAGACGTA 1502
DB |||||
1723 CGAGCTGTGGTACTTCTGGGGGGCCACGCTGTTTCATCTGATCTCTGTTTCATACAGACGTA 1782
QY |||||
1503 CTTTGAAGAACTCTCTTCTCTGTTCCAGGCCCTGCTCAAGTGGTGTCCAGGTGCTGTGTTT 1562
DB |||||

Db 1783 CTTTGAATCCTCTTCTCCAGGCCCTGCTCACAGTGTGTCCAGGTGCTGTGTTT 1842
Qy |||||
Db 1563 CTTGGCCATCGAGTGTGTA CTTGCCCTGCTGTGTGTCTGGCTGTGTGTGGCTGAA 1622
Qy |||||
Db 1843 CTTGGCCATCGAGTGTGTA CTTGCCCTGCTGTGTGTCTGGCTGTGTGTGGCTGAA 1902
Qy |||||
Db 1623 CTTGCTTTTACTATACACGTGGCTTCCAGACACAGGCATCTACAGTGTATGATCAGAA 1682
Qy |||||
Db 1903 CTTGCTTTTACTATACACGTGGCTTCCAGACACAGGCATCTACAGTGTATGATCAGAA 1962
Qy |||||
Db 1683 GGTTCATCTCGGGGACCTGCTGGCTTCTCTTCGATCTACTTACTTCTCTTTTCGGCTT 1742
Qy |||||
Db 1963 GGTTCATCTCGGGGACCTGCTGGCTTCTCTTCGATCTACTTACTTCTCTTTTCGGCTT 2022
Qy |||||
Db 1743 CGCTGTAGCCTCGTGTAGCCTGTAGCAGGAGGCTTGGCGCCCGAGAGCTCTACAGGCC 1802
Qy |||||
Db 2023 CGCTGTAGCCTCGTGTAGCCTGTAGCAGGAGGCTTGGCGCCCGAGAGCTCTACAGGCC 2082
Qy |||||
Db 1803 CAATGCCACAGAGTCAAGTGCAGCCCATGGAGGACAGGAGGAGGCAAGCGGGCCCA 1862
Db 2083 CAATGCCACAGAGTCAAGTGCAGCCCATGGAGGACAGGAGGAGGCAAGCGGGCCCA 2142
Qy |||||
Db 1863 GTACAGGGGTATCTCGAAGCCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGCGA 1922
Db 2143 GTACAGGGGTATCTCGAAGCCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGCGA 2202
Qy |||||
Db 1923 GCTGGCCTTCCAGAGCAGTGCATCTCCGCGGATGGTGTCTGTCTGTCTGTCTGTCTA 1982
Db 2203 GCTGGCCTTCCAGAGCAGTGCATCTCCGCGGATGGTGTCTGTCTGTCTGTCTGTCTA 2262
Qy |||||
Db 1983 CGTGTCTCACCTACATCTCTGTCTCAACATGCTCATCGCTCATGAGCGAGACCGT 2042
Db 2263 CGTGTCTCACCTACATCTCTGTCTCAACATGCTCATCGCTCATGAGCGAGACCGT 2322
Qy |||||
Db 2043 CAACAGTGTCCCACTCACAGCTGGAGCATCTGGAAGCTCGAAGAGCCATCTCTGTCT 2102
Db 2323 CAACAGTGTCCCACTCACAGCTGGAGCATCTGGAAGCTCGAAGAGCCATCTCTGTCT 2382
Qy |||||
Db 2103 GGAGATGGAGATGGCTATTGTTGGTGCAGAGACAGGAGCGGCGAGGTGTGATCTGAC 2162
Db 2383 GGAGATGGAGATGGCTATTGTTGGTGCAGAGAGAGAGCGGCGAGGTGTGATCTGAC 2442
Qy |||||
Db 2163 CGTTGGCACTAAGCCAGATGCGAGCCGAGTGGCTGTCTCAGGCTGAGGAGGT 2222
Db 2443 CGTTGGCACTAAGCCAGATGCGAGCCGAGTGGCTGTCTCAGGCTGAGGAGGT 2502
Qy |||||
Db 2223 GAACTGGCTTCATGGGAGCAGCGCTGCTTACGCTGTGTGAGGACCCGTCAGGGGCGAG 2282
Db 2503 GAACTGGCTTCATGGGAGCAGCGCTGCTTACGCTGTGTGAGGACCCGTCAGGGGCGAG 2562
Qy |||||
Db 2283 TGTCCCTCGAATCTCGAGAACCTGCTGTGGCTTCCCTCCCAAGGAGATGAGATGG 2342
Db 2563 TGTCCCTCGAATCTCGAGAACCTGCTGTGGCTTCCCTCCCAAGGAGATGAGATGG 2622
Qy |||||
Db 2343 TGCTCTCGAGAAATATGTCGCGCTCCAGCTCTCCAGTCCCACTGATGGCCACATG 2402
Db 2623 TGCTCTCGAGAAATATGTCGCGCTCCAGCTCTCCAGTCCCACTGATGGCCACATG 2682
Qy |||||
Db 2403 CAGCAGAGGCGCAGAGGACAGCAGAGGATCTTTTCAACACATCTGTCTGGCTCTGGG 2462
Db 2683 CAGCAGAGGCGCAGAGGACAGCAGAGGATCTTTTCAACACATCTGTCTGGCTCTGGG 2742
Qy |||||
Db 2463 TCCAGT 2469
Db 2743 TCCAGT 2749

RESULT 7
AAD09554
ID AAD09554 standard; cDNA; 2825 BP.
XX
AC AAD09554;
XX

DT 10-SEP-2001 (first entry)
XX Human transporter and ion channel-3 (TRICH-3) cDNA.

XX Human; transporter and ion channel-3; TRICH-3; vaccine; cystic fibrosis;
DE gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy;
XX hypertension; angina; neurological disorder; athma; bipolar disorder;
KW demantia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia;
KW Pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke;
KW Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy;
KW demyelinating disease; mental disorder; Schizophrenia; polymyositis;
KW muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease;
KW dermatomyositis; diabetes mellitus; immunological disorder; psoriasis;
KW rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus;
KW sickle cell anaemia; Wilson's disease; infertility; Cushing's disease;
KW scleroderma; pulmonary artery stenosis; nontropic; Addison's disease;
KW malabsorption syndrome; hypercholesterolaemia; cancer; 88.

XX Homo sapiens.

XX Key Location/Qualifiers
CDS 412..2706
FT /*tag= a
FT /product= "Human TRICH-3 protein"

PN WO200146258-A2.

XX 28-JUN-2001.

XX 22-DEC-2000; 2000WO-US035095.

XX 23-DEC-1999; 99US-0172000P.

XX 14-JAN-2000; 2000US-0176083P.

XX 21-JAN-2000; 2000US-0177332P.

XX 28-JAN-2000; 2000US-0178572P.

XX 02-FEB-2000; 2000US-0179758P.

XX 10-FEB-2000; 2000US-0181625P.

XX (INCY-) INCYTE GENOMICS INC.

XX Baughn MR, Burford N, Au-Young J, Lu DM, Yang J, Reddy R;

XX Lal P, Hillman JL, Azimzai Y, Yue H, Nguyen DB, Yao MG, Gandhi AR;

XX Tang YT, Khan FA;

XX WPI; 2001-418042/44.

XX P-PSDB; AAE04890.

XX Novel human transporter and ion channel proteins useful for treating and

XX preventing transport, neurological, muscle and immunological disorders.

XX Claim 5; Page 142-143; 160pp; English.

XX The present sequence is transporter and ion channel-3 (TRICH-3) cDNA.
XX TRICH is used as vaccine. TRICH is useful for treating a disease or
XX condition associated with decreased expression of functional TRICH, such
XX as transport disorder including amyotrophic lateral sclerosis, cystic
XX fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth disease,
XX Duchenne muscular dystrophy, angina and hypertension, neurological
XX disorders including Alzheimer's disease, amnesia, bipolar disorder,
XX dementia, depression, epilepsy, ischaemic cerebrovascular disease,
XX stroke, cerebral neoplasms, Pick's disease, Huntington's disease and
XX Parkinson's disease, demyelinating diseases, mental disorders including
XX mood anxiety, Schizophrenia and seasonal affective disorder, muscle
XX disorder including cardiomyopathy, myocarditis, polymyositis,
XX dermatomyositis, arrhythmias and asthma and immunological disorders
XX including AIDS, adult respiratory distress syndrome (ARDS), allergies,
XX anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's
XX syndrome, systemic lupus erythematosus and other diseases including
XX sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary
XX artery stenosis, Grave's disease, Cushing's disease, Addison's disease,
XX glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers
XX psoriasis and viral, bacterial, fungal, helminthic and protozoal
XX infections. TRICH DNA is useful in gene therapy and in diagnostic

Db 2358 CAAACAGTGTGCGCACTGACAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCT 2417
 Qy 2103 GGAGATGGAGATGGCTATTGGTGTGTCAGGAAGACGCGGCGAGGTGTGATGCTGAC 2162
 Db 2418 GGAGATGGAGATGGCTATTGGTGTGTCAGGAAGACGCGGCGAGGTGTGATGCTGAC 2477
 Qy 2163 CGTTGGCACTTAAGCCAGATGGCAGCCCGGATGAGCGCTGTGCTTCAGGGTGGAGAGGT 2222
 Db 2478 CGTTGGCACTTAAGCCAGATGGCAGCCCGGATGAGCGCTGTGCTTCAGGGTGGAGAGGT 2537
 Qy 2223 GAACCTGGCTTCATGGAGCAGACGCTGCTACGCTGTGTGAGGACCGGTTCAGGGCGAGG 2282
 Db 2538 GAACCTGGCTTCATGGAGCAGACGCTGCTACGCTGTGTGAGGACCGGTTCAGGGCGAGG 2597
 Qy 2283 TGTCCTCGAATCTCGAAGACCGTCTGCTGGCTTCCCTCCCAAGGAGATGAGATGG 2342
 Db 2598 TGTCCTCGAATCTCGAAGACCGTCTGCTGGCTTCCCTCCCAAGGAGATGAGATGG 2657
 Qy 2343 TGCTCTCGAGAAACCTATGTGCGCGTCCAGCTCTCCAGTCCAACTGATGGCCAGATG 2402
 Db 2658 TGCTCTCGAGAAACCTATGTGCGCGTCCAGCTCTCCAGTCCAACTGATGGCCAGATG 2717
 Qy 2403 CAGCAGAGCCGACAGAGCAGAGCAGAGGATCTTTCCAAACCATCTGCTGTGGG 2462
 Db 2718 CAGCAGAGCCGACAGAGCAGAGCAGAGGATCTTTCCAAACCATCTGCTGTGGG 2777
 Qy 2463 TCCAGT 2469
 Db 2778 TCCAGT 2784

RESULT 8
 ABL90839
 ID ABL90839 standard; cDNA; 2867 BP.
 XX ABL90839;
 XX 24-MAY-2002 (first entry)
 DT Human polynucleotide SEQ ID NO 1401.
 DE Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein; gene; ss.
 XX Homo sapiens.
 OS WO200190304-A2.
 PN 29-NOV-2001.
 XX 18-MAY-2001; 2001WO-US016450.
 XX 19-MAY-2000; 2000US-0205515P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Birse CE, Rosen CA;
 PI WPI; 2002-122018/16.
 DR P-PSDB; ABB90430.
 XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.
 XX Claim 4; SEQ ID NO 1401; 2081pp + Sequence Listing; English.
 PS The invention relates to novel genes (ABL89449-ABL90853) and proteins
 CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating

CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2867 BP; 589 A; 842 C; 826 G; 601 T; 0 U; 9 Other;
 Query Match 99.1%; Score 2447.4; DB 6; Length 2867;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2459; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
 Qy 3 CAGAGCCGACGCGCAGCTGGGAGGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG 62
 Db 303 CAACACCGACGCGCAGCTGGGAGGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG 362
 Qy 63 TCCTGGCTGACCGAGCAGCTCTCTCTCTAGGATGACCTCACCCCTCCAGCTCTCCAGT 122
 Db 363 TCCTGGCTGACCGAGCAGCTCTCTCTCTAGGATGACCTCACCCCTCCAGCTCTCCAGT 422
 Qy 123 TTTTCAGTTGGAGACATTAGATGGAGGCCAAGAAGATGGCTCTGAGCGGACAGAGAAA 182
 Db 423 TTTTCAGTTGGAGACATTAGATGGAGGCCAAGAAGATGGCTCTGAGCGGACAGAGAAA 482
 Qy 183 GCTGGATTTTGGAGCGGGCTGCTCCATGGAGTACAGTTCCAGGGCCAGAGCCGAA 242
 Db 483 GCTGGATTTTGGAGCGGGCTGCTCCATGGAGTACAGTTCCAGGGCCAGAGCCGAA 542
 Qy 243 ATTGCGCCCTCAGATAAGAGTCAACCTCACTACCGAAGGGAACAGGTGCCAGTCAAGCC 302
 Db 543 ATTGCGCCCTCAGATAAGAGTCAACCTCACTACCGAAGGGAACAGGTGCCAGTCAAGCC 602
 Qy 303 GGAATCCAAACCGATTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGTGTCCCGGA 362
 Db 603 GGAATCCAAACCGATTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGTGTCCCGGA 662
 Qy 363 GGAATCTGGTGGACTTCCAGAGTACCTGACAGACCCAGCAAGTACTCACCGACTCGGA 422
 Db 663 GGAATCTGGTGGACTTCCAGAGTACCTGACAGACCCAGCAAGTACTCACCGACTCGGA 722
 Qy 423 ATACACAGAGGGCTCCACAGGTAAGAGCTGCCCTGATGAAGCGTGTGCTGAACCTTAAGGA 482
 Db 723 ATACACAGAGGGCTCCACAGGTAAGAGCTGCCCTGATGAAGCGTGTGCTGAACCTTAAGGA 782
 Qy 483 CGGAGTCAATGCTGCAATCTGCCACTGTGTCAGATCGACAGGAGCTCTGGCAATCTCA 542
 Db 783 CGGAGTCAATGCTGCAATCTGCCACTGTGTCAGATCGACAGGAGCTCTGGCAATCTCA 842
 Qy 543 GCCCTGGTAAATGCCAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCACAT 602
 Db 843 GCCCTGGTAAATGCCAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCACAT 902
 Qy 603 CGCCNTTGAAGAGAGGAGTCTGCAGTGTGTGAAGCTCTCTGTGAGAAATGGGGCAATGT 662
 Db 903 CGCCNTTGAAGAGAGGAGTCTGCAGTGTGTGAAGCTCTCTGTGAGAAATGGGGCAATGT 962
 Qy 663 GCATGCCCGGGCTTGGCGCGCTTCTTCCAGAGGGCCAAAGGGAATTTTATTTTCGG 722
 Db 963 GCATGCCCGGGCTTGGCGCG- CGCTTCTTCCAGAGGGCCAAAGGGAATTTTATTTTCGG 1021
 Qy 723 TGAGCTACCCCTCTCTTTTGGCGCTTGGACCAAGCAGTGGGATGTGTAGCTACCTCTCT 782
 Db 1022 TGAGCTACCCCTCTCTTTTGGCGCTTGGACCAAGCAGTGGGATGTGTAGCTACCTCTCT 1081

1644	Db	CTCATGCTGTGACGGGCCACATCCTTATCTGCTAGGGGGGATCTACCTCTCTGTTGG	1703
1443	Qy	CCAGCTGTGGTACTTCTTGGGGGGCCACAGCTGTTTCACTGATCTCGTTCATAGACAGCTA	1502
1704	Db	CCAGCTGTGGTACTTCTTGGGGGGCCACAGCTGTTTCACTGATCTCGTTCATAGACAGCTA	1763
1503	Qy	CTTTGAAATCCTCTTCTCTGTTTCCAGGGCCCTGCTCACAGTGGTGTCCAGAGTGTGTGTTT	1562
1764	Db	CTTTGAAATCCTCTTCTCTGTTTCCAGGGCCCTGCTCACAGTGGTGTCCAGAGTGTGTGTTT	1823
1563	Qy	CCTGGCCATCGAGTGGTACTTGGCCCCCTGCTTGTGTGTCTGCGCTGGTGTCTGGGCTGGCTGAA	1622
1824	Db	CCTGGCCATCGAGTGGTACTTGGCCCCCTGCTTGTGTGTGTCTGCGCTGGTGTCTGGGCTGGCTGAA	1883
1623	Qy	CCTGCTTTACTATACAGCTGGCTTCCAGCACACAGGCATCTACAGTGTCTCATGTATCCAGAA	1682
1884	Db	CCTGCTTTACTATACAGCTGGCTTCCAGCACACAGGCATCTACAGTGTCTCATGTATCCAGAA	1943
1683	Qy	GGTCATCTCTGGGGACCTGCTGCGCTTCTTCTGATCTACTTACTTCTCTCTTTTTCGGCTT	1742
1944	Db	GGTCATCTCTGGGGACCTGCTGCGCTTCTTCTGATCTACTTACTTCTCTCTTTTTCGGCTT	2003
1743	Qy	CGCTGTAGCCCTGTGTGAGCTGTGACAGAGGCTTGGGGCCCCGAAAGCTCTTACAGGCCC	1802
2004	Db	CGCTGTAGCCCTGTGTGAGCTGTGACAGAGGCTTGGGGCCCCGAAAGCTCTTACAGGCCC	2063
1803	Qy	CAATGCCACAGAGTCAGTGCAGGCCATCTGAGGGACAGAGGACAGAGGCAACGGGGCCCA	1862
2064	Db	CAATGCCACAGAGTCAGTGCAGGCCATCTGAGGGACAGAGGACAGAGGCAACGGGGCCCA	2123
1863	Qy	GTACAGGGGTATCTCTGGAAGCCTCTTGGAGCTCTTCAAATTCACCATCGCATGGGCGA	1922
2124	Db	GTA CAGGGGTATCTCTGGAAGCCTCTTGGAGCTCTTCAAATTCACCATCGCATGGGCGA	2183
1923	Qy	GCTGGCCTTCCAGAGCAGCTGTCACTTCCGGGCAATGGTGTGTGTGTGTGTGTGGCCTA	1982
2184	Db	GCTGGCCTTCCAGAGCAGCTGTCACTTCCGGGCAATGGTGTGTGTGTGTGTGTGGCCTA	2243
1983	Qy	CGTCTGTCTACCTACATCTCTGCTGTCTCAATGCTCATCGCCCTCATGAGCGAGACCGT	2042
2244	Db	CGTCTGTCTACCTACATCTCTGCTGTCTCAATGCTCATCGCCCTCATGAGCGAGACCGT	2303
2043	Qy	CAACAGTGTCCGCCATGACAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCTCT	2102
2304	Db	CAACAGTGTCCGCCATGACAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCTCT	2363
2103	Qy	GGAGATGAGAAATGGCTATTGGTGGTGCAGAGAGAGAGCGGGCAGGTGTGTGATGCTGTAC	2162
2364	Db	GGAGATGAGAAATGGCTATTGGTGGTGCAGAGAGAGAGCGGGCAGGTGTGTGATGCTGTAC	2423
2163	Qy	CGTTGGCACTAAGCCAGATGCGACCCGGATGAGCGTGTGTCTTACGGGTGGAGGAGGT	2222
2424	Db	CGTTGGCACTAAGCCAGATGCGACCCGGATGAGCGTGTGTCTTACGGGTGGAGGAGGT	2483
2223	Qy	GAACTGGGCTTTCATGGGAGCAGACGCTGCCCTACGCTGTGTGAGGACCCGTCAGGGGCGG	2282
2484	Db	GAACTGGGCTTTCATGGGAGCAGACGCTGCCCTACGCTGTGTGAGGACCCGTCAGGGGCGG	2543
2283	Qy	TGTCCTCTGAACTCTCGAGAAACCTGTCTGGCTTCCCTTCCCAAGGAGGATGAGGATGG	2342
2544	Db	TGTCCTCTGAACTCTCGAGAAACCTGTCTGGCTTCCCTTCCCAAGGAGGATGAGGATGG	2603
2343	Qy	TGCTCTGAGGAAACTATGTGCCCCCTCCAGTCTCTCAGTCCAACTGATGGCCCCAGATG	2402
2604	Db	TGCTCTGAGGAAACTATGTGCCCCCTCCAGTCTCTCAGTCCAACTGATGGCCCCAGATG	2663
2403	Qy	CAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCCAAACCACTATCTGCTGGCTCTGGG	2462
2664	Db	CAGCAGGAGGCCAGAGGACAGAGCAGAGGATCTTTTCCAAACCACTATCTGCTGGCTCTGGG	2723
2463	Qy	TCCCAGT 2469	

Db 2724 TCCAGT 2730

RESULT 10
AAA14874
ID AAA14874 standard; DNA; 2765 BP.
XX
AC AAA14874;
XX
XX 08-AUG-2000 (first entry)
XX
DE DNA encoding a vanilloid receptor-like (VR-L) protein.
XX
XX Cation channel protein; vanilloid receptor-like 1 protein; VR-L;
KW noxious heat; pain; inflammation; tissue damage; nociception;
KW gene therapy; sensory neuron; immune system; analgesic; immunomodulatory;
KW neuromodulatory; ss.
XX
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX CDS 358..2652
XX FT /*tag= a
XX FT /product= "vanilloid receptor-like (VR-L) protein"
XX FT /transl_except= (pos: 802..804, aa: Gly)
XX FT /transl_except= (pos: 955..957, aa: Lys)
XX FT /transl_except= (pos: 2035..2037, aa: Thr)
XX FT /transl_except= (pos: 2356..2358, aa: Xaa)
XX FT /note= "Xaa is an unspecified amino acid"
XX
PN W0200022121-A2.
XX
XX 20-APR-2000.
XX
XX 08-OCT-1999; 99WO-CB003348.
XX
XX 09-OCT-1998; 98GB-00022124.
XX
XX (UNLO) UNIV COLLEGE LONDON.
XX
XX Garcia R, Wood JN, England S;
XX WPI; 2000-317978/27.
XX P-PSDB; AAY84834.
XX
XX Novel non-selective cation channel protein and nucleotides useful as
XX screening agents and in gene therapy of disorders associated with sensory
XX neurons and leucocytes such as pain, autoimmune disorders and leukemia.
XX
XX Claim 5; Fig 3A; 55pp; English.
XX
XX The present sequence encodes a non-selective cation channel protein,
XX designated vanilloid receptor-like 1 (VR-L). The protein is obtained from,
XX human T lymphocytes. The VR-L protein is activated by noxious heat, and
XX is not capsaicin sensitive. VR-L is expressed in sensory neurons, and is
XX likely to play a role in mediating the pain and inflammation accompanying
XX tissue damage (nociception). The VR-L polynucleotide is useful for
XX influencing the electrophysiological and/or pharmacological properties of
XX a cell, and is also useful in the gene therapy treatment of disorders
XX associated with sensory neurons and/or cells of the immune system and
XX also for the preparation of a medicament for use in gene therapy. The VR-
XX L polynucleotides and polypeptides are useful for identifying a substance
XX with ion-channel modulating activity (such as analgesics), or compounds
XX which affect nociception, immunomodulatory agents, neuromodulatory agents
XX
XX SQ Sequence 2765 BP; 560 A; 821 C; 792 G; 589 T; 0 U; 3 Other;

Query Match 98.4%; Score 2428.8; DB 3; Length 2765;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2442; Conservative 0; Mismatches 25; Indels 0; Gaps 0

3 CGAGGCCGACGGCGAGCTGGGAGGAGACAGGACCTTGACATCTCCATCTGCACAGG 62
|||||

Db	264	CAACACCGACGCGCAGCTGCTGGAGGAAAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG	323
Qy	63	TCCTGGCTGACCGAGCAGCCTCTCTCTCTAGATGACCTCACCCCTCCAGCTCTCCAGT	122
Db	324	TT	383
Qy	123	TTTCAGGTTGGAGACATTAGATGGAGCCCAAGAGATGGCTCTTGAGCGGACAGAGGAAA	182
Db	384	TTTTCAGGTTGGAGACATTAGATGGAGCCCAAGAGATGGCTCTTGAGCGGACAGAGGAAA	443
Qy	183	GCTGGATTTTGGAGCGGGCTGCTCTCCATGGAGTACAGTTCCAGGGCGAGACCGGAA	242
Db	444	GCTGGATTTTGGAGCGGGCTGCTCTCCATGGAGTACAGTTCCAGGGCGAGACCGGAA	503
Qy	243	ATTGCGCCCTCAGATAGAGTCAACCTCAACTACCGAAAGGAAACAGGTCGCCAGTCAGCC	302
Db	504	ATTGCGCCCTCAGATAGAGTCAACCTCAACTACCGAAAGGAAACAGGTCGCCAGTCAGCC	563
Qy	303	GGATCCAAACCGATTTGACCGAGATCGGCTCTTCAATGCGGCTCTCCCGGGGTGTCCCCGA	362
Db	564	GGATCCAAACCGATTTGACCGAGATCGGCTCTTCAATGCGGCTCTCCCGGGGTGTCCCCGA	623
Qy	363	GGATCTGGCTGGACTTCCAGAGTACCTGAGGAAAGACAGCAAGTACTCAACGACTCGGA	422
Db	624	GGATCTGGCTGGACTTCCAGAGTACCTGAGGAAAGACAGCAAGTACTCAACGACTCGGA	683
Qy	423	ATACACAGAGGGCTCCACAGGTAAGAGTGCCTGATGAAGGCTGTGCTGAACCTTAAGGA	482
Db	684	ATACACAGAGGGCTCCACAGGTAAGAGTGCCTGATGAAGGCTGTGCTGAACCTTAAGGA	743
Qy	483	CGGAGTCAATGCGCTGCAATCTGCGACCTGCTGCAGATCGACAGGAGCTCTGGCAATCTCA	542
Db	744	CGGAGTCAATGCGCTGCAATCTGCGACCTGCTGCAGATCGACAGGAGCTCTGGCAATCTCA	803
Qy	543	GCCCTCGTAAATGCCAGTGCAAGATGACTATTACCGAGGCGACAGCGCTCTGCACAT	602
Db	804	GCCCTCGTAAATGCCAGTGCAAGATGACTATTACCGAGGCGACAGCGCTCTGCACAT	863
Qy	603	CGCATTTGAGAAAGGAGTCTGACGTGTGAGAGCTCTCGTGAGAGTGGGGCCCAATGT	662
Db	864	CGCATTTGAGAAAGGAGTCTGACGTGTGAGAGCTCTCGTGAGAGTGGGGCCCAATGT	923
Qy	663	GCATGCCGGGCGCTCGGCGCTCTTCCAGAGGGGCAAGGGAGCTTGTCTTTTATTTGG	722
Db	924	GCATGCCGGGCGCTCGGCGCTCTTCCAGAGTGGCAAGGAGCTTGTCTTTTATTTGG	983
Qy	723	TGAGCTACCCCTCTCTTTTGGCGCTTGACCAAGCAGTGGGATGTGTAAGTACTCTCCT	782
Db	984	TGAGCTACCCCTCTCTTTTGGCGCTTGACCAAGCAGTGGGATGTGTAAGTACTCTCCT	1043
Qy	783	GGAGAACCCACACAGCGCGGCGCTGAGGCGCACTGACTCCCGAGGGGCAACAGTCTCT	842
Db	1044	GGAGAACCCACACAGCGCGGCGCTGAGGCGCACTGACTCCCGAGGGGCAACAGTCTCT	1103
Qy	843	GCATGCCCTAGTATGATCTCGGACAACTCAGCTGAGAAATTGCACTGGTGACACAGCAT	902
Db	1104	GCATGCCCTAGTATGATCTCGGACAACTCAGCTGAGAAATTGCACTGGTGACACAGCAT	1163
Qy	903	GTATGATGGGCTCTCCAAAGCTGGGGCGCGCTCTGCGCTTACCGTGAGCTTGAGGACAT	962
Db	1164	GTATGATGGGCTCTCCAAAGCTGGGGCGCGCTCTGCGCTTACCGTGAGCTTGAGGACAT	1223
Qy	963	CCGCAACTTGAGATCTCAGCCTCTGAGCTGGCGCGCGAGAGGGGCAAGATCGAGAT	1022
Db	1224	CCGCAACTTGAGATCTCAGCCTCTGAGCTGGCGCGCGAGAGGGGCAAGATCGAGAT	1283
Qy	1023	TTTCAGGCACATCTCGAGCGGGAGTTTTCAGGACTGAGCCACTTTTCCCGAAAGTTTCA	1082
Db	1284	TTTCAGGCACATCTCGAGCGGGAGTTTTCAGGACTGAGCCACTTTTCCCGAAAGTTTCA	1343
Qy	1083	CGAGTGTGTCTATGGGCGCTGCGGGGTGTGCTGTATGACCTGGCTCTGTGGACAGCTG	1142
Db	1344	CGAGTGTGTCTATGGGCGCTGCGGGGTGTGCTGTATGACCTGGCTCTGTGGACAGCTG	1403
Qy	1143	TGAGAGAACTCAGTGTGGAGATCATTTGCCCTTTTCAATTGCAAGAGCCCCGACCGACCG	1202
Db	1404	TGAGAGAACTCAGTGTGGAGATCATTTGCCCTTTTCAATTGCAAGAGCCCCGACCGACCG	1463
Qy	1203	AATGTCGTTTTTGGAGCCCCCTGAAACAACTGCTGAGCGGAAATGGGATCTGCTCATCCC	1262
Db	1464	AATGTCGTTTTTGGAGCCCCCTGAAACAACTGCTGAGCGGAAATGGGATCTGCTCATCCC	1523
Qy	1263	CAAGTTCTTTTAAACTCTCTGTGTAATCTGATCTACATGTTTTCATCTTCAACCCTGTTC	1322
Db	1524	CAAGTTCTTTTAAACTCTCTGTGTAATCTGATCTACATGTTTTCATCTTCAACCCTGTTC	1583
Qy	1323	CTACCATCAGCCCTACCTTGAAGAAGCAGGCGGCCCTCACTCTGAAAGCGAGGTTGGAAA	1382
Db	1584	CTACCATCAGCCCTACCTTGAAGAAGCAGGCGGCCCTCACTCTGAAAGCGAGGTTGGAAA	1643
Qy	1383	CTCCATGCTGTGACGGGGCCACATCTTATCTCTGCTAGGGGGGATCTACTCTCTGTGGG	1442
Db	1644	CTCCATGCTGTGACGGGGCCACATCTTATCTCTGCTAGGGGGGATCTACTCTCTGTGGG	1703
Qy	1443	CCAGCTGTGTAATCTCTGCTGCGGCGCCACGTTGTTTCACTCTGATCTCTGTTTATACAG	1502
Db	1704	CCAACTGTGTAATCTCTGCTGCGGCGCCACGTTGTTTCACTCTGATCTCTGTTTATACAG	1763
Qy	1503	CTTTGAAATCTCTCTCTGTTCCAGGCCCTGCTCAGAGTGGTCTCCAGGCTGCTGTGTTT	1562
Db	1764	CTTTGAAATCTCTCTCTGTTCCACTCTGCTCAGAGTGGTCTCCAGGCTGCTGTGTTT	1823
Qy	1563	CTTGGCCATCGAGTGTAATCTGCGCCCTGCTGTTGTTCTGCGCTGGTGGCTGGCTGAA	1622
Db	1824	CTTGGCCATCGAGTGTAATCTGCGCCCTGCTGTTGTTCTGCGCTGGTGGCTGGCTGAA	1883
Qy	1623	CTTGGCTTTACTATACAGTGGCTTCCAGCACACAGGATCTTACAGTGTCAATGATCCAGAA	1682
Db	1884	CTTGGCTTTACTATACAGTGGCTTCCAGCACACAGGATCTTACAGTGTCAATGATCCAGAA	1943
Qy	1683	GGTCATCTCGCGGGAATCTGCGCTTCTCTCTGATCTACTTAGTCTTCTTTTTCGCTT	1742
Db	1944	GGTCATCTCGCGGGAATCTGCGCTTCTCTCTGATCTACTTAGTCTTCTTTTTCGCTT	2003
Qy	1743	CGCTGAGCCCTGAGCTGAGCCAGGAGCTTGGCGCCCGGAGCTCTTACAGGCC	1802
Db	2004	CGCTGAGCCCTGAGCTGAGCCAGGAGCTTGGCGCCCGGAGCTCTTACAGGCC	2063
Qy	1803	CAATGCCACAGATCAGTGCAGCCCATGGAGGACAGGAGGACGAGGGCAACCGGGCCCA	1862
Db	2064	CAATGCCACAGATCAGTGCAGCCCATGGAGGACAGGAGGACGAGGGCAACCGGGCCCA	2123
Qy	1863	GTACAGGGGTATCTTGGAGAGCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGCGGA	1922
Db	2124	GTACAGGGGTATCTTGGAGAGCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGCGGA	2183
Qy	1923	GCTGGCCTTCCAGGAGCAGCTGACCTTCCCGCGCATGGTGTCTGCTGTGCTGGCCTTA	1982
Db	2184	GCTGGCCTTCCAGGAGCAGCTGACCTTCCCGCGCATGGTGTCTGCTGTGCTGGCCTTA	2243
Qy	1983	CGTGTGCTCACCCTACATCTCTGCTCTCAACATGCTCTCATCGCCCTCATGAGCGAGACCGT	2042
Db	2244	CGTGTGCTCACCCTACATCTCTGCTCTCAACATGCTCTCATCGCCCTCATGAGCGAGACCGT	2303
Qy	2043	CAACAGTGTCCGACCTGACAGCTGGAGCATCTTGGAGCTCTTGGAGAGCCATCTCTGTCTCT	2102
Db	2304	CAACAGTGTCCGACCTGACAGCTGGAGCATCTTGGAGAGCCATCTTGTCTCTCT	2363
Qy	2103	GGAGATGGAGAAATGGCTATTGGTGTGAGGAAAGACAGCGGGCAGGTTGTGATGTGAC	2162
Db	2364	GGAGATGGAGAAATGGCTATTGGTGTGAGGAAAGACAGCGGGCAGGTTGTGATGTGAC	2423
Qy	2163	CGTGTGCACTAAGCCAGATGGCGAGCCCGGATGAGCGCTGTGCTTCAAGGTTGAGGAGGT	2222
Db	2424	CGTGTGCACTAAGCCAGATGGCGAGCCCGGATGAGCGCTGTGCTTCAAGGTTGAGGAGGT	2483

QY	661	GTGCATGCCCGCGCTGCGCGCTTCTTCCAGAAAGGCGCAAGGACATGTGCTTTATTTTC	720
Db	947	GTGCATGCCCGCGGCTGCGCGCTTCTTCCAGAAAGGCGCAAGGACATGTGCTTTATTTTC	1006
QY	721	GGTGAGCTACCCCTCTCTTTTGGCGCTTGACCAAGCAGTGGGATGTGGTAAGTACCTC	780
Db	1007	GGTGAGCTACCCCTCTCTTTTGGCGCTTGACCAAGCAGTGGGATGTGGTAAGTACCTC	1066
QY	781	CTGGAGAACCCACACAGCGCGGACGCTGCGAGGCACTGACTCCAGGGCAACACAGTC	840
Db	1067	CTGGAGAACCCACACAGCGCGGACGCTGCGAGGCACTGACTCCAGGGCAACACAGTC	1126
QY	841	CTGCATGCCCTAGTGATGATCTCGGCAACTCAGCTGAGAAATTTGCACTGCTGACACAGC	900
Db	1127	CTGCATGCCCTAGTGATGATCTCGGCAACTCAGCTGAGAAATTTGCACTGCTGACACAGC	1186
QY	901	ATGTATGATGGGCTCTCCAAAGCTGGGGCCGCTCTGCCCTTACCGTGAGCTTGAAGAC	960
Db	1187	ATGTATGATGGGCTCTCCAAAGCTGGGGCCGCTCTGCCCTTACCGTGAGCTTGAAGAC	1246
QY	961	ATCCGCAACTGAGAGATCTCAGCCCTCTGAAGCTGGCGCCGCAAGGAGGGCAAGATCGAG	1020
Db	1247	ATCCGCAACTGAGAGATCTCAGCCCTCTGAAGCTGGCGCCGCAAGGAGGGCAAGATCGAG	1306
QY	1021	ATTTTCAGGCACATCTGCAGCGGGAGTTTTCAGGACTGAGCACCTTTTCCGAAAGTTC	1080
Db	1307	ATTTTTCAGGCACATCTGCAGCGGGAGTTTTCAGGACTGAGCACCTTTTCCGAAAGTTC	1366
QY	1081	ACCGAGTGTGTATGGGCTGTCCGGGTGTGCTGTATGACTTGGCTTCTGTGGACAGC	1140
Db	1367	ACCGAGTGTGTATGGGCTGTCCGGGTGTGCTGTATGACTTGGCTTCTGTGGACAGC	1426
QY	1141	TGTGAGAGAACTCAGTGTGAGATCATTTGCCCTTTTCATTGCAAGAGCCCGCACAGCAC	1200
Db	1427	TGTGAGAGAACTCAGTGTGAGATCATTTGCCCTTTTCATTGCAAGAGCCCGCACAGCAC	1486
QY	1201	CGAATGCTGTTTGGAGCCCTTGAACAACTGCTGCAGCGCAATGGGATCTGCTCATC	1260
Db	1487	CGAATGCTGTTTGGAGCCCTTGAACAACTGCTGCAGCGCAATGGGATCTGCTCATC	1546
QY	1261	CCCAAGTCTTCTTAAACTTCTGTGTATCTGATCTACATGTTTCACTTTCACCGCTGT	1320
Db	1547	CCCAAGTCTTCTTAAACTTCTGTGTATCTGATCTACATGTTTCACTTTCACCGCTGT	1606
QY	1321	GCCTACCATCAGGCTACCTTGAAAGACAGGCGCGCCCTTCACTGAAAGCGAGGTTGGA	1380
Db	1607	GCCTACCATCAGGCTACCTTGAAAGACAGGCGCGCCCTTCACTGAAAGCGAGGTTGGA	1663
QY	1381	AACCTCATGCTGACGGCGCACATCTTATCTCTAGGGGGATCTACCTCTCGTG	1440
Db	1664	AACCTCATGCTGACGGCGCACATCTTATCTCTAGGGGGATCTACCTCTCGTG	1723
QY	1441	GGCCAGCTGTGTAATTTCTGGCGCGCCAGCTGTTTCACTTGGATCTCTGTTTATAGACAGC	1500
Db	1724	GGCCAGCTGTGTAATTTCTGGCGCGCCAGCTGTTTCACTTGGATCTCTGTTTATAGACAGC	1783
QY	1501	TACTTTGAAATPCTTCTTCTGTTTCCAGGCGCTGCTCACAGTGGTGTCCAGGTGTGTGT	1560
Db	1784	TACTTTGAAATPCTTCTTCTGTTTCCAGGCGCTGCTCACAGTGGTGTCCAGGTGTGTGT	1843
QY	1561	TTCTGGCCATCGAGTGGTACCTGCCCTGCTTGTCTGCGCTGGTGTGGCTGGCTG	1620
Db	1844	TTCTGGCCATCGAGTGGTACCTGCCCTGCTTGTCTGCGCTGGTGTGGCTGGCTG	1903
QY	1621	AACCTGCTTTTACTATACAGTGGCTTCCAGCACACAGGATCTACAGTGTATGATCCAG	1680
Db	1904	AACCTGCTTTTACTATACAGTGGCTTCCAGCACACAGGATCTACAGTGTATGATCCAG	1963
QY	1681	AAGGTCACTCTCGCGGACCTGCTGCGCTTCTTCTGATCTACTTCTTCTTTTGGC	1740
Db	1964	AAGGTCACTCTCGCGGACCTGCTGCGCTTCTTCTGATCTACTTCTTCTTTTGGC	2023

XX US2003022289-A1.
PN 30-JAN-2003.
XX 03-MAY-2002; 2002US-00137316.
PF 11-AUG-1998; 98US-00132316.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Young PE, Ruben SM;
XX MPI; 2003-540138/51.
DR P-PSDB; ABO42807.
XX
PT New nucleic acid molecule encoding vanilloid receptor 2 polypeptides,
PT useful for drug screening and for diagnosing, preventing or treating
PT disorders such as chronic pain syndromes, inflammation, ischemia or
PT autoimmune diseases.
XX
XX Claim 4; Fig 1; 82pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
XX vanilloid receptor-2 polypeptide. The composition and methods are useful
XX for drug screening and for diagnosing, preventing or treating disorders
XX such as chronic pain syndromes, congenital pain insensitivity, arthritis,
XX inflammation, ischaemia (e.g. stroke or myocardial infarction), host
XX defence dysfunction, immune surveillance dysfunction, neurodegenerative
XX disorders (e.g. Alzheimer's disease or Parkinson's disease), multiple
XX sclerosis, infections (e.g. viral including AIDS), autoimmunity (e.g.
XX systemic lupus erythematosus), septic shock, liver disease, cachexia,
XX anorexia, immune dysfunction or allergy. The nucleic acid may also be
XX used for gene mapping or chromosome identification. The present sequence
XX represents cDNA encoding the human vanilloid receptor-2
XX
SQ Sequence 2805 BP; 579 A; 830 C; 803 G; 593 T; 0 U; 0 Other;

Query Match 98.2%; Score 2424.6; DB 9; Length 2805;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2455; Conservative 0; Mismatches 9; Indels 5; Gaps 2;

QY 3 CGAGGCGGCGCGAGTGGGAGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG 62
DB 287 CAACACCGACGCGACGTTGGGAGGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG 346

QY 63 TCCTGGCTGGACCGAGC--AGCCTCTCTCTCTAGGATGACCTCACCCCTCCAGCTCTCCA 120
DB 347 TCCTGGCTGGACCGAGCTATGCTCTCTCTCTAGGATGACCTCACCCCTCCAGCTCTCCA 406

QY 121 GTTTTCAGGTTGGAGACATTAGATGGAGGCCAAGAGATGGCTCTGAGGCGGACAGAGGA 180
DB 407 GTTTTCAGGTTGGAGACATTAGATGGAGGCCAAGAGATGGCTCTGAGGCGGACAGAGGA 466

QY 181 AAGCTGGATTTTGGAGCGGGCTCCCTCCATGGAGTCAAGTTCACGGGCGGACCGG 240
DB 467 AAGCTGGATTTTGGAGCGGGCTCCCTCCATGGAGTCAAGTTCACGGGCGGACCGG 526

QY 241 AAATTGCGCCCTCAGATAAGAGTCAACTCACTACCGAAAGGGAACAGGTGGCCAGTTCAG 300
DB 527 AAATTGCGCCCTCAGATAAGAGTCAACTCACTACCGAAAGGGAACAGGTGGCCAGTTCAG 586

QY 301 CCGGATCCAAACCGATTGACCGAGATCGGCTCTTCAATCGGCTCTCCCGGGGTTGCC 360
DB 587 CCGGATCCAAACCGATTGACCGAGATCGGCTCTTCAATCGGCTCTCCCGGGGTTGCC 646

QY 361 GAGGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACCAAGTACCTCACCGACTCG 420
DB 647 GAGGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACCAAGTACCTCACCGACTCG 706

QY 421 GAATACACAGAGGGCTCCACAGGTAAAGACGTGCTGATGAAGGTGCTGCTGAAACCTTAAG 480
DB 707 GAATACACAGAGGGCTCCACAGGTAAAGACGTGCTGATGAAGGTGCTGCTGAAACCTTAAG 766

QY 481 GACGGAGTCAATGCCTGCAATCTTCCCACTGCTGCAGATCGACAGGGACTCTGGCAATCCT 540
DB 767 GACGGGGTCAATGCTGCAATCTTGCACATGCTGCAGATCGACCGGACTCTGGCAATCCT 826

QY 541 CAGCCCTCGTAAATGCCAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCAC 600
DB 827 CAGCCCTCGTAAATGCCAGTGCACAGATGACTATTACCGAGGCCACAGCGCTCTGCAC 886

QY 601 ATCGCATTTGAGAAGAGGAGTCTGCAGTGTGTGAAGTCTCTGTGTGAAGATGGGGCAAT 660
DB 887 ATCGCATTTGAGAAGAGGAGTCTGCAGTGTGTGAAGTCTCTGTGTGAAGATGGGGCAAT 946

QY 661 GTGCATGCCCGGGCCCTGCGGCCCTTCTTCAGAGAGGCCAAGGGACTTGTCTTTATTTTC 720
DB 947 GTGCATGCCCGGGCCCTGCGGCCCTTCTTCAGAGAGGCCAAGGGACTTGTCTTTATTTTC 1006

QY 721 GGTGAGCTACCCCTCTCTTTGGCCGCTTGCACCAAGCAGTGGATGTGCTAAAGCTACCTC 780
DB 1007 GGTGAGCTACCCCTCTCTTTGGCCGCTTGCACCAAGCAGTGGATGTGCTAAAGCTACCTC 1066

QY 781 CTGGAGAACCCACACAGCCGCCAGCTCTGCAGGCCACTGACTCCAGGGCAACAGATC 840
DB 1067 CTGGAGAACCCACACAGCCGCCAGCTCTGCAGGCCACTGACTCCAGGGCAACAGATC 1126

QY 841 CTGCATGCCCTAGTGTATGATCTCGCAACTCAGCTGAGAACATTGCACTGGTGACCAGC 900
DB 1127 CTGCATGCCCTAGTGTATGATCTCGCAACTCAGCTGAGAACATTGCACTGGTGACCAGC 1186

QY 901 ATGTATGATGGGCTCTCTCAAGCTGGGGCCGCTCTGCCCTACCGTGCAGCTTGAAGGAC 960
DB 1187 ATGTATGATGGGCTCTCTCAAGCTGGGGCCGCTCTGCCCTACCGTGCAGCTTGAAGGAC 1246

QY 961 ATCCGCAACCTTCAGGATCTCACGCTCTGAAGTGTGGCCGCAAGAGAGGCAAGATCGAG 1020
DB 1247 ATCCGCAACCTTCAGGATCTCACGCTCTGAAGTGTGGCCGCAAGAGAGGCAAGATCGAG 1306

QY 1021 ATTTTCAGGCACATCTCTCAGCGGGAGTTTTCAGGATGAGGCACCTTTCCGAAAGTTTC 1080
DB 1307 ATTTTCAGGCACATCTCTCAGCGGGAGTTTTCAGGATGAGGCACCTTTCCGAAAGTTTC 1366

QY 1081 ACCGAGTGTGTATGGGCTCTCGGGTGTGCTGTATGACCTGTGCTCTGTGGACAGC 1140
DB 1367 ACCGAGTGTGTATGGGCTCTCGGGTGTGCTGTATGACCTGTGCTCTGTGGACAGC 1426

QY 1141 TGTGAGGAGAACTCAGTGTGGAGATCATGTGCTTTTCATTGCAAGAGCCGCAACCCAGC 1200
DB 1427 TGTGAGGAGAACTCAGTGTGGAGATCATGTGCTTTTCATTGCAAGAGCCGCAACCCAGC 1486

QY 1201 CGAATGGTGTGTTTGGAGCCCTGCAAACTGCTGCAGCGGAAATGGGATCTGCTCATC 1260
DB 1487 CGAATGGTGTGTTTGGAGCCCTGCAAACTGCTGCAGCGGAAATGGGATCTGCTCATC 1546

QY 1261 CCCAAGTCTCTTAACTTCTGTGTAATCTGATCTATGATCTTCACTTCTTCACTGCTGTT 1320
DB 1547 CCCAAGTCTCTTAACTTCTGTGTAATCTGATCTATGATCTTCACTTCTTCACTGCTGTT 1606

QY 1321 GCTTACCATCAGCCTACCTGAAAGAGAGCGGCCCTTCACTGAAAGCGGAGGTTGGA 1380
DB 1607 GCTTACCATCAGCCTACCTGAAAGAGAGCGGCCCTTCACTGAAAGCGGAGGTTGGA 1663

QY 1381 AACTCCATGCTGCTGAGGGGCCACATCTTATCTCTAGGGGGATCTACCTCTCTCGTG 1440
DB 1664 AACTCCATGCTGCTGAGGGGCCACATCTTATCTCTAGGGGGATCTACCTCTCTCGTG 1723

QY 1441 GGCAGCTGTGTGTAATCTTCTGGGGGCCACAGTGTTCATCTGATCTCTGTTTCATAGACAGC 1500
DB 1724 GGCAGCTGTGTGTAATCTTCTGGGGGCCACAGTGTTCATCTGATCTCTGTTTCATAGACAGC 1783

QY 1501 TACTTTGAAATCCTCTTCTGTTTCCAGGCCCTGCTCACAGTGTGTGTTCCAGGTGCTGTGT 1560
DB 1784 TACTTTGAAATCCTCTTCTGTTTCCAGGCCCTGCTCACAGTGTGTGTTCCAGGTGCTGTGT 1843

QY	1561	TTCTGCGCCATCGAGTGGTATCACTGCCCCTGCTTGTGTCTGCGCTGCTGTGCTGGGCTGGCTG	1620
DB	1844	TTCTGCGCCATCGAGTGGTATCACTGCCCCTGCTTGTGTCTGCGCTGCTGTGCTGGGCTGGCTG	1903
QY	1621	AACCTGCTTTTACTATATACACGTGGCTTCCAGCACACAGGCATCTTACAGTGTCAATGATCCAG	1680
DB	1904	AACCTGCTTTTACTATATACACGTGGCTTCCAGCACACAGGCATCTTACAGTGTCAATGATCCAG	1963
QY	1681	AAGGTCACTCTTCGCGGACCTGCTGCGCTTCCTTCTGATCTTACTTGTCTTCTTTTTCGGC	1740
DB	1964	AAGGTCACTCTTCGCGGACCTGCTGCGCTTCCTTCTGATCTTACTTGTCTTCTTTTTCGGC	2023
QY	1741	TTGCTGTAGCCCTGTTGAGCCTGAGCCAGGAGGCTTTGGCGCCCGAGAGCTCTTACAGGC	1800
DB	2024	TTGCTGTAGCCCTGTTGAGCCTGAGCCAGGAGGCTTTGGCGCCCGAGAGCTCTTACAGGC	2083
QY	1801	CCCAATGCCACAGAGTCAAGTGCACGCCATCGAGGGACAGGAGACAGAGGCCAACGGGGCC	1860
DB	2084	CCCAATGCCACAGAGTCAAGTGCACGCCATCGAGGGACAGGAGACAGAGGCCAACGGGGCC	2143
QY	1861	CAGTACAGGGGTATCTCTGGAAAGCCTCTCTGGAGCTTTTCAAAATTCAACATCGGCATGGGC	1920
DB	2144	CAGTACAGGGGTATCTCTGGAAAGCCTCTCTGGAGCTTTTCAAAATTCAACATCGGCATGGGC	2203
QY	1921	GAGCTGGCCTTCAGAGGACGACTGCATCTTCGGCGGCATGTGTCTGCTGCTGCTGCGCC	1980
DB	2204	GAGCTGGCCTTCAGAGGACGACTGCATCTTCGGCGGCATGTGTCTGCTGCTGCTGCGCC	2263
QY	1981	TACGTGCTGCTCACTACATCCTGCTGCTCAACATGCTCATTCGCCCTCATGAGCGAGACCC	2040
DB	2264	TACGTGCTGCTCACTACATCCTGCTGCTCAACATGCTCATTCGCCCTCATGAGCGAGACCC	2323
QY	2041	GTCAAACAGTGTGCGCACCTGCAGCTGGAGCATCTTGGAAAGCTGCGAAAGCCATCTCTGTCT	2100
DB	2324	GTCAAACAGTGTGCGCACCTGCAGCTGGAGCATCTTGGAAAGCTGCGAAAGCCATCTCTGTCT	2383
QY	2101	CTGGAGATGGAGATATGGCTATTTGTGTGTGAGGAAAGACAGCGGGCAGCTGTGATGCTCTG	2160
DB	2384	CTGGAGATGGAGATATGGCTATTTGTGTGTGAGGAAAGACAGCGGGCAGCTGTGATGCTCTG	2443
QY	2161	ACCGTTGACACTTAAGCCACAGATGGACCGCCGATCAGCGCTGGTGCTTTTCAAGGTGGAGGAG	2220
DB	2444	ACCGTTGACACTTAAGCCACAGATGGACCGCCGATCAGCGCTGGTGCTTTTCAAGGTGGAGGAG	2503
QY	2221	GTGAACCTGGCTTTCA TGGGAGCAGACGCTGCTACGCTGTGTGAGGACCCGCTCAGGGGCA	2280
DB	2504	GTGAACCTGGCTTTCA TGGGAGCAGACGCTGCTACGCTGTGTGAGGACCCGCTCAGGGGCA	2563
QY	2281	GGTGTCCCTCGAACTCTCGAGAACCTGTCTGTGGCTTCCCTCCCAAGGAGGATGAGGAT	2340
DB	2564	GGTGTCCCTCGAACTCTCGAGAACCTGTCTGTGGCTTCCCTCCCAAGGAGGATGAGGAT	2623
QY	2341	GGTGTCTCTGAGGAAAACCTATGTGCGCGCTCCAGCTCTCTCCAGTCCAACTGATGCCCCAGA	2400
DB	2624	GGTGTCTCTGAGGAAAACCTATGTGCGCGCTCCAGCTCTCTCCAGTCCAACTGATGCCCCAGA	2683
QY	2401	TGCAGCAGGAGGCCAGAGGACAGACAGAGGATCTTTTCCAAACCACTCTGTGTGCTCTGG	2460
DB	2684	TGCAGCAGGAGGCCAGAGGACAGACAGAGGATCTTTTCCAAACCACTCTGTGTGCTCTGG	2743
QY	2461	GGTCCCAAGT	2469
DB	2744	GGTCCCAAGT	2752

RESULT 13

ADP09695

ID ADP09695 standard; cDNA; 2507 bp.

XX
AC ADP09695:XX
XX
XXXXXX

DT 29-JUL-2004 (first entry)

X

DE	Human VRL-1 cDNA.
XX	
XX	Human; ulcerative colitis; CHI3L2; DUOX2; VRL-1; IL17R; GRO1; GRO3; gene;
KW	ss; antiulcer; antiinflammatory.
XX	
XX	Homo sapiens.
OS	
XX	
XX	Key Location/Qualifiers
FT	CDS 166..2460
FT	/*tag= a
FT	/product= "Human VRL-1"
FT	
XX	
XX	JP2004135545-A.
XX	
XX	13-MAY-2004.
XX	
PD	16-OCT-2002; 2002JP-00302030.
XX	
PD	16-OCT-2002; 2002JP-00302030.
XX	
XX	16-OCT-2002; 2002JP-00302030.
XX	
XX	(SUMU) SUMITOMO SEIYAKU KK.
XX	
XX	WPI: 2004-360954/34.
XX	P-PSDB; ADP09701.
XX	
DR	Novel disease marker of ulcerative colitis, has polynucleotide of CHI3L2
XX	gene, DUOX2 gene, VRL-1 gene, IL17R gene, GRO1 gene, or GRO3 gene and
PT	antibody recognizing CHI3L2, DUOX2, VRL-1, IL17R, GRO1, or GRO3.
PT	
XX	
XX	Disclosure; SEQ ID NO 3; 142pp; Japanese.
XX	
XX	The invention relates to a disease marker of ulcerative colitis,
XX	comprising a polynucleotide which has at least 15 continuous bases of the
CC	CHI3L2 gene, DUOX2 gene, VRL-1 gene, IL17R gene, GRO1 gene or GRO3 gene
CC	and/or an antibody recognising a CHI3L2, DUOX2, VRL-1, IL17R, GRO1 or
CC	GRO3 polypeptide. The invention also relates to a method of screening for
CC	a test substance capable of suppressing the expression, function or
CC	activity of the CHI3L2 gene, DUOX2 gene, VRL-1 gene, IL17R gene, GRO1
CC	gene or GRO3 gene, involving contacting the cell expressing the gene with
CC	the test substance, and a therapeutic agent for ulcerative colitis
CC	comprising a substance capable of suppressing the expression, function or
CC	activity of any one of the genes. The disease marker is useful as a probe
CC	or primer in detection of ulcerative colitis and for screening for
CC	therapeutic agents for ulcerative colitis. The genes are useful for
CC	treating ulcerative colitis. This sequence represents cDNA encoding the
CC	human VRL-1 polypeptide of the invention.

Query Match	97.1%	Score 2397.8;	DB 12;	Length 2507;
Best Local Similarity	99.0%;	Pred. No. 0;		
Matches 2411: Conservative	0;	Mismatches 25;	Indels 0;	Gaps 0;

Qy	3	CGAGGCGGACGCGAGCTGGGAGGAGACAGGACCTTTGACATCTCCATCTGCACAGG	62
Db	72	CAACACGACGGGAGCTGGAGGAGACAGGACCTTGAATCTCCATCTGCACAGG	131
Qy	63	TCCTGGGTGACCGGAGGAGCGCTCTCTCTTAGATGACCTCACTCCAGCTCTCCAGT	122
Db	132	TCCTGGGTGACCGGAGGAGCGCCCTCTCTCTTAGATGACCTCACTCCAGCTCTCCAGT	191
Qy	123	TTTCAGGTTTGGAGACATTTAGATGAGGCGCCAAGAAAGATGGCTCTGAGGCGGACAGAGGAAA	182
Db	192	TTTCAGGTTTGGAGACATTTAGATGAGGCGCCAAGAAAGATGGCTCTGAGGCGGACAGAGGAAA	251
Qy	183	GCTGGATTTTGGGAGCGGGTGCTCCCTCCATGGAGTCAAGTTCCAGGCGGAGGACCGGAA	242
Db	252	GCTGGATTTTGGGAGCGGGTGCTCCCTCCATGGAGTCAAGTTCCAGGCGGAGGACCGGNA	311
Qy	243	ATTCCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAAGGGAAACAGTGCAGCTCAGCC	302
Db	312	ATTCCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAAGGGAAACAGTGCAGCTCAGCC	371

Db 1141 ||||| CCCCCTGAACAACTGCTGCAGGCGAAATGGGATCTGCTCATCCCGCAAGTTCTTCTTAAC 1200
Qy 1279 TTCCCTGTGTAATCTGATCTACATGTTTCATCTTCACCGCTGTGTGCTTACCATCAGCCTACC 1338
Db 1201 TTCCCTGTGTAATCTGATCTACATGTTTCATCTTCACCGCTGTGTGCTTACCATCAGCCTACC 1260
Qy 1339 CTGAAGAAGCAGGCCGCCCTCACCTGAAAGCGGAGGTTGGAACTCCATGCTGCTGAGC 1398
Db 1261 CTGAAGAAGCAGGCCGCCCTCACCTGAAAGCGGAGGTTGGAACTCCATGCTGCTGAGC 1320
Qy 1399 GGCACATCTTATCTGCTAGGGGGAATCTACTCTCTGTGTGGCCAGCTGTGTTACTTC 1458
Db 1321 GGCACATCTTATCTGCTAGGGGGAATCTACTCTCTGTGTGGCCAGCTGTGTTACTTC 1380
Qy 1459 TGGCGGCGGCACGCTGTTTCATCTGATCTCGTTTCATAGACAGCTACTTTGAAATCTCTTC 1518
Db 1381 TGGCGGCGGCACGCTGTTTCATCTGATCTCGTTTCATAGACAGCTACTTTGAAATCTCTTC 1440
Qy 1519 CTGTTCCAGGCCCTGCTCAAGTGTGTCCAGGTGCTGTGTTTCTTGCCCAATCGAGTGG 1578
Db 1441 CTGTTCCAGGCCCTGCTCAAGTGTGTCCAGGTGCTGTGTTTCTTGCCCAATCGAGTGG 1500
Qy 1579 TACTCGCCCTGCTGTGTTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1638
Db 1501 TACTCGCCCTGCTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Qy 1639 CGTGGCTTCCAGCACACAGGCATCTACAGTGTCTATGATCCAGAGGTCTCTCGCGGAC 1698
Db 1561 CGTGGCTTCCAGCACACAGGCATCTACAGTGTCTATGATCCAGAGGTCTCTCGCGGAC 1620
Qy 1699 CTGCTGCGCTTCTCTGATCTACTTAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1758
Db 1621 CTGCTGCGCTTCTCTGATCTACTTAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1680
Qy 1759 AGCCTGAGCAGAGGCTTGGCGCCCGCGAAGCTCTACAGGCCCGCAATGCCACAGAGTCA 1818
Db 1681 AGCCTGAGCAGAGGCTTGGCGCCCGCGAAGCTCTACAGGCCCGCAATGCCACAGAGTCA 1740
Qy 1819 GTCCAGCCCATGAGGACAGAGGAGCAGGGGCAACGGGGCCAGTACAGGGGTATCTCTG 1878
Db 1741 GTCCAGCCCATGAGGACAGAGGAGCAGGGGCAACGGGGCCAGTACAGGGGTATCTCTG 1800
Qy 1879 GAAGCCTCTCTGGAGCTCTTCAAATTCACCATCGGCATGGCGAGCTGGCTTCCAGGAG 1938
Db 1801 GAAGCCTCTCTGGAGCTCTTCAAATTCACCATCGGCATGGCGAGCTGGCTTCCAGGAG 1860
Qy 1939 CAGCTGCATCTCCGGCGCATGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1998
Db 1861 CAGCTGCATCTCCGGCGCATGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Qy 1999 ATCTGCTGCTCAACATGCTCATCGCCTCATCAGCGAGACCGTCAACAGTGTGCGCACT 2058
Db 1921 ATCTGCTGCTCAACATGCTCATCGCCTCATCAGCGAGACCGTCAACAGTGTGCGCACT 1980
Qy 2059 GACAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTGTCTCTGGAGATGGAGATGGC 2118
Db 1981 GACAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTGTCTCTGGAGATGGAGATGGC 2040
Qy 2119 TATTGTGTGTGAGGAAGACGCGGCGAGTGTGATGTGACCGTGGACCTAAGCCA 2178
Db 2041 TATTGTGTGTGAGGAAGACGCGGCGAGTGTGATGTGACCGTGGACCTAAGCCA 2100
Qy 2179 GATGGCAGCCGATGAGCGCTGTGCTTCCAGGCTGAGGAGTGAACCTGGGCTTCATGG 2238
Db 2101 GATGGCAGCCGATGAGCGCTGTGCTTCCAGGCTGAGGAGTGAACCTGGGCTTCATGG 2160
Qy 2239 GAGCAGACGCTGCTAGCTGTGTGAGGACCCCGTCAAGGGCAGGTGTCTCTCGAATCTTC 2298
Db 2161 GAGCAGACGCTGCTAGCTGTGTGAGGACCCCGTCAAGGGCAGGTGTCTCTCGAATCTTC 2220
Qy 2299 GAGAACCTGTCTGGCTTCCCTCCAGGAGGATGAGATGGTGGCTCTGAGGAAC 2358

Db 2221 GAGAACCCCTGTCTCTGGCTTCCCTCCCAAGGAGGATGAGGATGGTGCCTCTCAGGNAAC 2280
Qy 2359 TATGTGCCCGTCCAGCTCTCTCCAGTCCCACTGATGCCAGATCAGCAGGAGGCCAGAG 2418
Db 2281 TATGTGCCCGTCCAGCTCTCTCCAGTCCCACTGATGCCAGATCAGCAGGAGGCCAGAG 2340
Qy 2419 GACAGACGAGGATCTTTCCAAACACATCTGCTGCTCT 2458
Db 2341 GACAGACGAGGATCTTTCCAAACACATCTGCTGCTCT 2380

RESULT 15
AAZ07114
ID AAZ07114 standard; cDNA; 2351 BP.
XX
AC AAZ07114;
DT 08-OCT-1999 (first entry)
XX
DE Human vanilloid receptor homologue VANILREP2 encoding cDNA.
XX
KW Human; vanilloid receptor homologue; VANILREP2; polymorphic variant;
KW PVP-1; therapy; diagnosis; chronic pain; neuropathic; postoperative;
KW rheumatoid arthritis; neuralgia; algesia; nerve injury; ischaemia;
KW neurodegeneration; stroke; incontinence; inflammatory disorder; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
CDS 5..2299
FT /*tag= a
FT /product= "VANILREP2"
FT /note= "vanilloid receptor homologue"
XX
PN WO937765-A1.
XX
PD 29-JUL-1999.
XX
PF 25-JAN-1999; 99WO-EP000420.
XX
PR 27-JAN-1998; 98EP-00300549.
PR 26-OCT-1998; 98GB-00023421.
PR 20-JAN-1999; 99GB-00001209.
XX
PA (SMIX) SMITHLINE BEECHAM PLC.
XX
PI Davis JB, Duckworth DM, Hayes PD;
XX
DR WPI; 1999-479049/40.
DR P-PSDB; AAY29469.
XX
PT New human vanilloid receptor homologues (VANILREP2).
XX
PS Claim 9; Page 29-30; 47pp; English.
XX
CC The present sequence encodes a human vanilloid receptor homologue,
CC designated VANILREP2. VANILREP2 can be used to diagnose disease or
CC susceptibility to disease related to expression or activity of VANILREP2
CC polypeptides. VANILREP2 may be used to treat diseases including pain,
CC (for example chronic, neuropathic, postoperative, rheumatoid arthritic),
CC neuralgia, algesia, nerve injury, ischaemia, neurodegeneration, stroke,
CC incontinence, and inflammatory disorders
XX
SQ Sequence 2351 BP; 486 A; 684 C; 676 G; 505 T; 0 U; 0 Other;

Query Match 95.1%; Score 2347.8; DB 2; Length 2351;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2349; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 93 TAGGATGACCTCACCTCCAGCTCTCCAGTTCAGTTGGAGACATTAGATGGAGGCCA 152
Db 1 TAGGATGACCTCACCTCCAGCTCTCCAGTTCAGTTGGAGACATTAGATGGAGGCCA 60

Qy	153	AGAAGTGGCTCTGAGGGGGACAGAGGAAAGCTGGAATTTTGGGAGCGGGCTGCTCCCAT	212	Db	1141	GCTGAGCGGAAATGGGATCTGCTCATCCCAAGTTCTTCTTAACTTCTGTTGTAATCT	1200
Db	61	AGAAGTGGCTCTGAGGGGGACAGAGGAAAGCTGGAATTTTGGGAGCGGGCTGCTCCCAT	120	Qy	1293	GATCTTACATGTTTCACTTTTCAACCGCTGTTCACACCTTACCTTACGCTTACCTTGAAGAAGCAGGC	1352
Qy	213	GGAGTTCACAGTTTCCAGGGCGAGGACCGGAAATTTGGCCCTCAGATAAGAGTCAACCTCAA	272	Db	1201	GATCTTACATGTTTCACTTTTCAACCGCTGTTCACACCTTACCTTACGCTTACCTTGAAGAAGCAGGC	1260
Db	121	GGAGTTCACAGTTTCCAGGGCGAGGACCGGAAATTTGGCCCTCAGATAAGAGTCAACCTCAA	180	Qy	1353	CGCCCTCACCTGAAAGGGGAGTGGAAACTCCATGCTGCTGACGGGCGACATCTCTTAT	1412
Qy	273	CTACCGAAAGGAAACAGGTGCCAGTCAAGTCAGCGGATCCAAACCGATTTTGACCGAGATCGGCT	332	Db	1261	CGCCCTCACCTGAAAGGGGAGTGGAAACTCCATGCTGCTGACGGGCGACATCTCTTAT	1320
Db	181	CTACCGAAAGGAAACAGGTGCCAGTCAAGTCAGCGGATCCAAACCGATTTTGACCGAGATCGGCT	240	Qy	1413	CCTGCTAGGGGGGATCTACCTCTCGTGGGCGACGCTGTGGTACTTCTTGGGCGGCGCACCGT	1472
Qy	333	CTTCAATGCGGTCTCCCGGGGTGTCCTCGAGGATCTGCTGAGATCTTCCAGAGTACCTGAG	392	Db	1321	CCTGCTAGGGGGGATCTACCTCTCGTGGGCGACGCTGTGGTACTTCTTGGGCGGCGCACCGT	1380
Db	241	CTTCAATGCGGTCTCCCGGGGTGTCCTCGAGGATCTGCGTGGACTTCCAGAGTACCTGAG	300	Qy	1473	GTTTCACTGGAATCTCGTTCTATAGACAGCTACTTTTGAATCTCTTCTTCTGTTTCAGGGCCCT	1532
Qy	393	CAAGACCAAGTACTCTCACCGACTCCGGAATACACAGAGGGCTCCACAGGTAAGACGTG	452	Db	1381	GTTTCACTGGAATCTCGTTCTATAGACAGCTACTTTTGAATCTCTTCTTCTGTTTCAGGGCCCT	1440
Db	301	CAAGACCAAGTACTCTCACCGACTCCGGAATACACAGAGGGCTCCACAGGTAAGACGTG	360	Qy	1533	GCTTACAGTGTGTGCCAGGTGCTGTTTCTTCTGGCCATCGAGTGGTACCTGCCCTGCT	1592
Qy	453	CCTGATGAAGGGTGTCTGAACTTTAAGGACGAGTCAATGCTGCAATTCCTGCCACTGCT	512	Db	1441	GCTTACAGTGTGTGCCAGGTGCTGTTTCTTCTGGCCATCGAGTGGTACCTGCCCTGCT	1500
Db	361	CCTGATGAAGGGTGTCTGAACTTTAAGGACGAGTCAATGCTGCAATTCCTGCCACTGCT	420	Qy	1593	TGTTGCTCGCTGGTGTGGCTGGCTGGCTGAACTCTTATATACACGTTGGCTTCAGACA	1652
Qy	513	GCAGATCGACAGGACTCTGGCAATCTTCAAGCCCTGCTGTAATGTCACAGTGCACAGATGA	572	Db	1501	TGTTGCTCGCTGGTGTGGCTGGCTGGCTGAACTCTTATATACACGTTGGCTTCAGACA	1560
Db	421	GCAGATCGACAGGACTCTGGCAATCTTCAAGCCCTGCTGTAATGTCACAGTGCACAGATGA	480	Qy	1653	CACAGGCACTTACAGTGTTCATGATCCAGAAAGGTCACTCTCGGGGACCTGCTGGCTTTCCT	1712
Qy	573	CTATTACGAGGCCACAGCGCTCTGCACATCCCAATTGAGAGGAGGTCTGCAAGTGT	632	Db	1561	CACAGGCACTTACAGTGTTCATGATCCAGAAAGGTCACTCTCGGGGACCTGCTGGCTTTCCT	1620
Db	481	CTATTACGAGGCCACAGCGCTCTGCACATCCCAATTGAGAGGAGGTCTGCAAGTGT	540	Qy	1713	TCGTATCTACTTAGTCTTCTTTTTCGGCTTCGCTGTAGCCCTGGTGGAGCCTTGAGCCAGGA	1772
Qy	633	GAAGCTCCTGGTGGGAAATGGGGCCAAATGTGCATGCCCGGGCTGCGGCCCTTCTTCCA	692	Db	1621	TCGTATCTACTTAGTCTTCTTTTTCGGCTTCGCTGTAGCCCTGGTGGAGCCTTGAGCCAGGA	1680
Db	541	GAAGCTCCTGGTGGGAAATGGGGCCAAATGTGCATGCCCGGGCTGCGGCCCTTCTTCCA	600	Qy	1773	GGCTTGGCGCCCGGAAGCTCTTACAGGCCCCAAATGCCACAGAGTCAGTGAGCCCATGGA	1832
Qy	693	GAAGGCGAAGGACTTGTCTTTTATTTTGGGTAGCTACCCCTCTCTTTTGGCGGTGGAC	752	Db	1681	GGCTTGGCGCCCGGAAGCTCTTACAGGCCCCAAATGCCACAGAGTCAGTGAGCCCATGGA	1740
Db	601	GAAGGCGAAGGACTTGTCTTTTATTTTGGGTAGCTACCCCTCTCTTTTGGCGGTGGAC	660	Qy	1833	GGGACAGGAGGACGAGGGCCAAACGGGGCCAGTACAGGGGTATCTGGAAGCCTCTCTTGGGA	1892
Qy	753	CAAGCATGGGATGGTAAAGCTTACTCTCTGAGAACCCACACAGCCCGCCAGCCTGCA	812	Db	1741	GGGACAGGAGGACGAGGGCCAAACGGGGCCAGTACAGGGGTATCTGGAAGCCTCTCTTGGGA	1800
Db	661	CAAGCATGGGATGGTAAAGCTTACTCTCTGAGAACCCACACAGCCCGCCAGCCTGCA	720	Qy	1893	GCTCTTCAAATTCACCATCGGATCGGGCGAGCTGGCTTCCAGAGGAGCTGCACTTCCG	1952
Qy	813	GGCCACTGACTCCACAGGCGAAACACAGTCTCTGCATGCCCTAGTGTATCTCGGACAACTC	872	Db	1801	GCTCTTCAAATTCACCATCGGATCGGGCGAGCTGGCTTCCAGAGGAGCTGCACTTCCG	1860
Db	721	GGCCACTGACTCCACAGGCGAAACACAGTCTCTGCATGCCCTAGTGTATCTCGGACAACTC	780	Qy	1953	CGGCAATGGTGTGCTGCTGCTGGCTTACGCTGCTGCTACCTACCTACCTACCTGCTGCTCAA	2012
Qy	873	AGCTGAGAACTTGCATCTGCTGACAGCATGATGATGAGTGGCTCTTCCAAAGCTGGGGCCG	932	Db	1861	CGGCAATGGTGTGCTGCTGCTGCTGGCTTACGCTGCTGCTACCTACCTACCTGCTGCTCAA	1920
Db	781	AGCTGAGAACTTGCATCTGCTGACAGCATGATGATGAGTGGCTCTTCCAAAGCTGGGGCCG	840	Qy	2013	CATGCTCATTCGCCCTCATGAGCGAGAACCGTCAACAGTGTGCTGCTGCTGAGAGCTGGAGAT	2072
Qy	933	CCTCTGCCCTTACGCTGACGTTGAGGACATCCGCAACCTGCAAGATCTCAGCCTCTGAA	992	Db	1921	CATGCTCATTCGCCCTCATGAGCGAGAACCGTCAACAGTGTGCTGCTGCTGAGAGCTGGAGAT	1980
Db	841	CCTCTGCCCTTACGCTGACGTTGAGGACATCCGCAACCTGCAAGATCTCAGCCTCTGAA	900	Qy	2073	CTGGAAGCTGCGAAGGCCATCTCTGCTCTGAGATGAGGAATCGCTATTTGGTGGTGCAG	2132
Qy	993	GCTGGCCGCAAGGAGGCGAAGATCGAGATTTTTCAGGCACTCTTCCAGCGGAGTTTTC	1052	Db	1981	CTGGAAGCTGCGAAGGCCATCTCTGCTCTGAGATGAGGAATCGCTATTTGGTGGTGCAG	2040
Db	901	GCTGGCCGCAAGGAGGCGAAGATCGAGATTTTTCAGGCACTCTTCCAGCGGAGTTTTC	960	Qy	2133	GAAGAGCAGCGGGCGAGGTGTGATGCTGACCGCTTGGCACTAAGCCAGATGTCAGCCCGGA	2192
Qy	1053	AGGACTGAGCCACTTTTCCGAAAGTTTCAACGAGTGGTCTATGGGCTGTGCGGGTGT	1112	Db	2041	GAAGAGCAGCGGGCGAGGTGTGATGCTGACCGCTTGGCACTAAGCCAGATGTCAGCCCGGA	2100
Db	961	AGGACTGAGCCACTTTTCCGAAAGTTTCAACGAGTGGTCTATGGGCTGTGCGGGTGT	1020	Qy	2193	TGAGCGCTGGTGTCTTCCAGGGTGGAGAGGTGAACCTGGGCTTTCATGGGAGCAGACGCTGCC	2252
Qy	1113	GCTGTATGACTGTGTCAGAGTGTG					

Db	2221	GGCTTCCCTCCCAAGGAGGATGAGGATGGTGCTCTGAGGAAAACATATGTGCCCGTCCA	2280
Qy	2373	GCTCTCTCCAGTCCCACTGATGGCCCAAGATGCACGAGGAGGCCACAGAGCAGAGGA	2432
Db	2281	GCTCCTCCAGTCCCACTGATGGCCCAAGATGCACGAGGAGGCCACAGAGCAGAGGA	2340
Qy	2433	TCTTTCCACC	2443
Db	2341	TCTTTCCACC	2351

Search completed: October 6, 2005, 17:58:53
Job time : 1233 secs

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 16:02:42 ; Search time 10359 Seconds
(without alignments)

11548.984 Million cell updates/sec

Title: US-09-445-614B-1

Perfect score: 2469

Sequence: 1 cagcaggcgagcgagcgtc.....gctggctcgggggtccagct 2469

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2462.2	99.7	2809	6	BD264279 Novel mem
2	2460.6	99.7	2797	9	BC018926 Homo sapi
3	2459	99.6	2780	9	BC051305 Homo sapi
4	2455.8	99.5	2825	6	AX179742 Sequence 1
5	2444.6	99.0	2783	6	A94121 Sequence 1
6	2444.6	99.0	2783	6	AX017826 Sequence
7	2428.8	98.4	2765	6	BD251411 Ion chann
8	2428.8	98.4	2765	6	AX023769 Sequence
9	2424.6	98.2	2805	6	AR225700 Sequence
10	2397.8	97.1	2507	9	AF103906 Homo sapi
11	2379.4	96.4	2397	9	AF129112 Homo sapi
12	2378.4	96.3	2380	6	AR181402 Sequence
13	2378.4	96.3	2380	6	BD131756 Nucleic a
14	2347.8	95.1	2351	6	AX019706 Sequence
15	2347.8	95.1	2351	6	BD130940 Human van
16	2347.8	95.1	2351	9	AJ487963 Homo sapi
17	2333.4	94.5	2348	6	AX019710 Sequence
18	2333.4	94.5	2348	6	BD130942 Human van
19	2292	92.8	2292	6	BD264280 Novel mem

20	2259.2	91.5	2779	6	BD191226	BD191226 186 human
21	2259.2	91.5	2779	6	AX924736	AX924736 Sequence
22	2061.8	83.5	2860	6	BD191342	BD191342 186 human
23	2061.8	83.5	2860	6	AX924852	AX924852 Sequence
24	1720	69.7	1790	6	AR220826	AR220826 Sequence
25	1581.2	64.0	2710	10	BC005415	BC005415 Mus muscu
26	1572	63.7	2824	10	AB021665	AB021665 Mus muscu
27	1571.2	63.6	2419	10	AY487844	AY487844 F-11 rat/
28	1522.4	61.7	2718	10	AF129113	AF129113 Rattus no
29	1522.4	61.7	2736	6	AR181381	AR181381 Sequence
30	1522.4	61.7	2736	6	BD081816	BD081816 Nucleic a
31	1522.4	61.7	2736	6	BD131735	BD131735 Nucleic a
32	1498	60.7	2713	10	AB029330	AB029330 Rattus no
33	1478.6	59.9	2890	10	AB022332	AB022332 Rattus no
34	1224.2	49.6	2126	6	BD156841	BD156841 Primer fo
35	1224.2	49.6	2126	6	AX877774	AX877774 Sequence
36	1224.2	49.6	2126	9	AK001896	AK001896 Homo sapi
37	1098.4	44.5	1794	6	BD264283	BD264283 Novel mem
38	1065.8	43.2	1662	6	BD264284	BD264284 Novel mem
39	1007.4	40.8	1489	6	BD264282	BD264282 Novel mem
40	1005.4	40.7	1308	6	AR181392	AR181392 Sequence
41	750.8	30.4	884	6	BD081827	BD081827 Nucleic a
42	750.8	30.4	884	6	BD131746	BD131746 Nucleic a
43	750.8	30.4	884	6	AX019708	AX019708 Sequence
44	750.4	30.4	885	6	AX019708	AX019708 Sequence
45	750.4	30.4	885	6	BD130941	BD130941 Human van

ALIGNMENTS

RESULT 1

BD264279

LOCUS

DEFINITION

Novel members of protein

utilization thereof.

ACCESSION

BD264279

VERSION

BD264279.1 GI:33074047

KEYWORDS

JP 2002531069-A/3.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 2809)

AUTHORS

Curtis,R.A.J.

TITLE

Novel members of protein

utilization thereof

JOURNAL

Patent: JP 2002531069-A 3

COMMENT

MILLENNIUM PHARMACEUTICALS INC

OS

JP 2002531069-A/3

PD

24-SEP-2002

PF

12-NOV-1999 JP 2000582560

PR

13-NOV-1998 US 60/108322,28-DEC-1998 US 60/114078 PR

26-FEB-1999 US 09/258633,19-OCT-1999 US 09/421134 PI RORY A

J CURTIS

PC

C12N15/09,A61K45/00,A61P25/04,C07K14/705,C07K16/28,C07K19/00,

PC

C12N1/15,

PC

C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/02,C12Q1/68 PC

PC

C12N1/15,G01N33/50,

PC

G01N33/53,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC Novel

members of protein capsaicin/vanilloid receptor family CC

and

CC utilization thereof

FT

Key

Location/Qualifiers

FT

CDS

1..2809

Location/Qualifiers

(361)..(2652).

FEATURES

source

1..2809

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 99.7%; Score 2462.2; DB 6; Length 2809;									
Best Local Similarity 99.9%; Pred. No. 0;									
Matches 2464; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
QY	3	CGAGGCGGACGCGCAGCTGGGAGGAAGACAGGACCCTTGACATCTCCATCTGCACAGAGG	62						
DB	267	CAACACGACGCGCAGCTGGAGGAAGACAGGACCTTGACATCTCAATCTGCACAGAGG	326						
QY	63	TCCTGGCTGGACCGAGCAGCTCCTCCTCTAGGATGACCTCACTCCAGCTCTCCAGT	122						
DB	327	TCCTGGCTGGACCGAGCAGCTCCTCCTCTAGGATGACCTCACTCCAGCTCTCCAGT	386						
QY	123	TTTTCAGGTTGGACACATTAGATGGAGCCCAAGAGATGCTCTGAGCGGACAGAGAA	182						
DB	387	TTTTCAGGTTGGACACATTAGATGGAGCCCAAGAGATGCTCTGAGCGGACAGAGAA	446						
QY	183	GCTGGATTTTGGAGCGGGCTGCTCCCATGGAGTCACTGATTCACAGGGCGAGACCGGAA	242						
DB	447	GCTGGATTTTGGAGCGGGCTGCTCCCATGGAGTCACTGATTCACAGGGCGAGACCGGAA	506						
QY	243	ATTCGCCCTTCAGATAAGAGTCAACCTCAACTACCGAAAGGGAACAGGTGCCAGTCAGCC	302						
DB	507	ATTCGCCCTTCAGATAAGAGTCAACCTCAACTACCGAAAGGGAACAGGTGCCAGTCAGCC	566						
QY	303	GGATCCAAACCGATTTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCGCCGA	362						
DB	567	GGATCCAAACCGATTTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCGCCGA	626						
QY	363	GGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACCAAGTACTCTACCGACTCCGGA	422						
DB	627	GGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACCAAGTACTCTACCGACTCCGGA	686						
QY	423	ATACACAGAGGGTCCACAGGTGAAGCTGCTGATGAAGCTGTGCTGAACCTTAAAGGA	482						
DB	687	ATACACAGAGGGTCCACAGGTGAAGCTGCTGATGAAGCTGTGCTGAACCTTAAAGGA	746						
QY	483	CGAGTCAATGCCCTGCATTTCTGCCACTGCTGCHAGATCGACNGGACTCTGGCAATCTCA	542						
DB	747	CGAGTCAATGCCCTGCATTTCTGCCACTGCTGCHAGATCGACAGGGACTCTGGCAATCTCA	806						
QY	543	GCCCTTGGTAAATGCCCAGTGACAGATGACTATTACCGAGGGCCACAGCGCTCTGCACAT	602						
DB	807	GCCCTTGGTAAATGCCCAGTGACAGATGACTATTACCGAGGGCCACAGCGCTCTGCACAT	866						
QY	603	CGCCATTGAGAAGAGGATCTGCAGTGTGTGAAGCTCTGCTGAGAAATGGGGCCCAATGT	662						
DB	867	CGCCATTGAGAAGAGGATCTGCAGTGTGTGAAGCTCTGCTGAGAAATGGGGCCCAATGT	926						
QY	663	GCAATGCCGGGCTTGCGGCGCTTCTTCCAGAAAGGGCCAGGACTTGCTTTTATTTCGG	722						
DB	927	GCAATGCCGGGCTTGCGGCGCTTCTTCCAGAAAGGGCCAGGACTTGCTTTTATTTCGG	986						
QY	723	TGAGCTACCCCTCTCTTTTGGCCGCTTGACAAAGCAGTGGGATGTGTGAAGCTTACCTCCT	782						
DB	987	TGAGCTACCCCTCTCTTTTGGCCGCTTGACAAAGCAGTGGGATGTGTGAAGCTTACCTCCT	1046						
QY	783	GGAGAACCCACACAGCCGCCAGCTGACAGGCCACTGACTCCAGGGCAACACAGTCCT	842						
DB	1047	GGAGAACCCACACAGCCGCCAGCTGACAGGCCACTGACTCCAGGGCAACACAGTCCT	1106						
QY	843	GCAATGCCCTTGTGATGATCTCGACACTCAGCTGAGAACATTGCACTGGTGACCAAGCAT	902						
DB	1107	GCAATGCCCTTGTGATGATCTCGACACTCAGCTGAGAACATTGCACTGGTGACCAAGCAT	1166						
QY	903	GTAATGAGGCTCTCTCAAGCTGGGGCCCGCTCTGCCCCTACCGCTGAGCTTTCAGGACAT	962						
DB	1167	GTAATGAGGCTCTCTCAAGCTGGGGCCCGCTCTGCCCCTACCGCTGAGCTTTCAGGACAT	1226						
QY	963	CCGCAACCTGCAGGATCTCAAGCTCTGAAGCTGGCGGCCCAAGAGGGCAAGATTCAGAT	1022						
DB	1227	CCGCAACCTGCAGGATCTCAAGCTCTGAAGCTGGCGGCCCAAGAGGGCAAGATTCAGAT	1286						
QY	1023	TTTCAGGCACATCTCTGCAGCGGGGTTTTCAGGACTGAGGCCACTTTCCCGAAGATTCTAC	1082						

DB	1287	TTTCAGGCACATCTCTGCAGCGGGAGTTTTCAGACTGAGCCACTTTCCCGAAGATTCTAC	1346						
QY	1083	CGAGTGGTGTCTATAGGCGCTGTCCGGGTGTGCTGTATGACCTGGCTTCTGTGACAGCTG	1142						
DB	1347	CGAGTGGTGTCTATAGGCGCTGTCCGGGTGTGCTGTATGACCTGGCTTCTGTGACAGCTG	1406						
QY	1143	TCAGGAGAACTCAGTGTGGAGATCATTTGCCCTTTCAATTCAGAGCCCGCACCGACACCG	1202						
DB	1407	TCAGGAGAACTCAGTGTGGAGATCATTTGCCCTTTCAATTCAGAGCCCGCACCGACACCG	1466						
QY	1203	AATGTGCTTTTGGAGCCCTGAAACAACTGCTGACGGCGAAATGGGATCTGCTCATCC	1262						
DB	1467	AATGTGCTTTTGGAGCCCTGAAACAACTGCTGACGGCGAAATGGGATCTGCTCATCC	1526						
QY	1263	CAAGTCTCTTAAACTTCTCTGTGTAATCTGATCTACATGTTCACTTCCCGCTGTGCTG	1322						
DB	1527	CAAGTCTCTTAAACTTCTCTGTGTAATCTGATCTACATGTTCACTTCCCGCTGTGCTG	1586						
QY	1323	CTACCATCAGCCTACCTTGAAGAGCAGGCGCCCTCACCTGAAAGCGGAGGTTGGAAA	1382						
DB	1587	CTACCATCAGCCTACCTTGAAGAGCAGGCGCCCTCACCTGAAAGCGGAGGTTGGAAA	1646						
QY	1383	CTCCATGCTGTGACGGGCCACATCCTTATCTGCTAGGGGGGATCTACCTCTCTGCTGG	1442						
DB	1647	CTCCATGCTGTGACGGGCCACATCCTTATCTGCTAGGGGGGATCTACCTCTCTGCTGG	1706						
QY	1443	CCAGCTGTGTTACTTCTGGCGGCCACGTTGTTCACTGGAATCTCGTTCAATGACAGCTA	1502						
DB	1707	CCAGCTGTGTTACTTCTGGCGGCCACGTTGTTCACTGGAATCTCGTTCAATGACAGCTA	1766						
QY	1503	CTTTGAAATCCTTCTCTGTTTCCAGGCCCTGCTCAAGTGGTGTCCAGGTGCTGTGTT	1562						
DB	1767	CTTTGAAATCCTTCTCTGTTTCCAGGCCCTGCTCAAGTGGTGTCCAGGTGCTGTGTT	1826						
QY	1563	CTGGCCATCTGAGTGTACTGCCCCTGCTGTGTCTGCGCTGGTGTGGCTGGCTGAA	1622						
DB	1827	CTGGCCATCTGAGTGGTACTGCCCCTGCTGTGTCTGCGCTGGTGTGGCTGGCTGAA	1886						
QY	1623	CCTGCTTTACTATAACGTTGCTTCCAGCACACAGGCACTACAGTGTCAATGATCAGAA	1682						
DB	1887	CCTGCTTTACTATAACGTTGCTTCCAGCACACAGGCACTACAGTGTCAATGATCAGAA	1946						
QY	1683	GGTCACTCTGCGGACCTGCTGCGCTTCTTCTGATCTACTTACTTCTTCTTCTGGCTT	1742						
DB	1947	GGTCACTCTGCGGACCTGCTGCGCTTCTTCTGATCTACTTACTTCTTCTTCTGGCTT	2006						
QY	1743	CGCTGAGCCCTGGTGAGCTGAGCCAGGAGGCTTGGCGCCCGAAGCTCTCTACAGGCC	1802						
DB	2007	CGCTGAGCCCTGGTGAGCTGAGCCAGGAGGCTTGGCGCCCGAAGCTCTCTACAGGCC	2066						
QY	1803	CAATGCCACAGAGTCACTGACAGCCCATGAGGAGGACAGGAGGCAACGCGGGCCCA	1862						
DB	2067	CAATGCCACAGAGTCACTGACAGCCCATGAGGAGGACAGGAGGCAACGCGGGCCCA	2126						
QY	1863	GTACAGGGGTATCTTGGAGCCCTCTTGGAGCTCTTCAAAATTCACCATCGGATGGCGCA	1922						
DB	2127	GTACAGGGGTATCTTGGAGCCCTCTTGGAGCTCTTCAAAATTCACCATCGGATGGCGCA	2186						
QY	1923	GCTGGCCTTCCAGGAGCAGCTGCACTTCCCGCGCATGGTGTGCTGCTGCTGCTGCTGCTA	1982						
DB	2187	GCTGGCCTTCCAGGAGCAGCTGCACTTCCCGCGCATGGTGTGCTGCTGCTGCTGCTGCTA	2246						
QY	1983	CGTGTGCTCACTACATCTCTGCTGCTCAATGCTCATCGCCCTCATGAGGAGACCGT	2042						
DB	2247	CGTGTGCTCACTACATCTCTGCTGCTCAATGCTCATCGCCCTCATGAGGAGACCGT	2306						
QY	2043	CAACAGTGTGCGCACTGACAGCTGAGCATCTGGAGCTGACAGAGCCATCTCTCTCT	2102						
DB	2307	CAACAGTGTGCGCACTGACAGCTGAGCATCTGGAGCTGACAGAGCCATCTCTCTCT	2366						
QY	2103	GGAGATGGAGAAATGGCTATTGCTGTGACAGGAAGACAGCGGCGCAGGTGTGATGCTGAC	2162						

QY	243	ATTGCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAGGGAACAGGTGCCAGTCAGCC	302	Db	1582	CTACCATCAGCCCTACCTGNAAGAGAGGCGCCCTCACCTGAAAGCGAGGTTGGAAA	1641
Db	502	ATTGCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAGGGAACAGGTGCCAGTCAGCC	561	QY	1383	CTCCATGCTGCTAGCGGGCCACATCCTTATCTCTGTAGGGGGATCTACTCTCTCGTGGG	1442
QY	303	GGATCCAAACCGATTGTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCGCCGA	362	Db	1642	CTCCATGCTGCTAGCGGGCCACATCCTTATCTCTGTAGGGGGATCTACTCTCTCGTGGG	1701
Db	562	GGATCCAAACCGATTGTGACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCGCCGA	621	QY	1443	CGAGCTGTGTTACTTCTGCGGGCGCCACGTGTTTCATCTGGATCTCGTTCATAGACAGCTA	1502
QY	363	GGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACCAGCAAGTACTCAACGACTCGGA	422	Db	1702	CCAGCTGTGTTACTTCTGCGGGCGCCACGTGTTTCATCTGGATCTCGTTCATAGACAGCTA	1761
Db	622	GGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACCAGCAAGTACTCAACGACTCGGA	681	QY	1503	CTTTGAAATCCCTCTTCTGTTCCAGGCCCTGTCTCACAGTGGTGTCCAGGTGTCTGTGTTT	1562
QY	423	ATACACAGAGGGCTCCACAGGTAAGAGCTGCTGTATGAAGGCTGTGCTGAACCTTAAAGGA	482	Db	1762	CTTTGAAATCCCTCTTCTGTTCCAGGCCCTGTCTCACAGTGGTGTCCAGGTGTCTGTGTTT	1821
Db	682	ATACACAGAGGGCTCCACAGGTAAGAGCTGCTGTATGAAGGCTGTGCTGAACCTTAAAGGA	741	QY	1563	CCTGGCCAPCGAGTGGTACCTGCCCTGTGTTGTCTGCGCTGGTGTCTGGGTGGCTGAA	1622
QY	483	CGAGGTCAAATGCCCTGCATCTGCGCACTGTCTGCAGATCGACAGGAGTCTTGGCAATCCTCA	542	Db	1822	CCTGGCCATCGAGTGGTACCTGCCCTGTGTTGTCTGCGCTGGTGTCTGGGTGGCTGAA	1881
Db	742	CGAGGTCAAATGCCCTGCATCTGCGCACTGTCTGCAGATCGACAGGAGTCTTGGCAATCCTCA	801	QY	1623	CCTGCTTTACTATACACGTGGCTTCCAGCACACAGGCCATCTACAGTGTCAATGATCCAGAA	1682
QY	543	GCCCTTGTTAAATGCCCAAGTGCAAGATGACTATTAACGAGGCCACAGCGCTCTGCACAT	602	Db	1882	CCTGCTTTTATATACACGTGGCTTCCAGCACACAGGCCATCTACAGTGTCAATGATCCAGAA	1941
Db	802	GCCCTTGTTAAATGCCCAAGTGCAAGATGACTATTAACGAGGCCACAGCGCTCTGCACAT	861	QY	1683	GGTCACTCTGCGGACCTGCTGCGCTTCTCTGATCTACTTACTTCTCTTTTCGGCTT	1742
QY	603	CGCATTTGAGAACAGAGTCTGACGTGTGTGAAGCTCCTGGTGGAGATGGGGCCCAATGT	662	Db	1942	GGTCACTCTGCGGACCTGCTGCGCTTCTCTGATCTACTTACTTCTCTTTTCGGCTT	2001
Db	862	CGCATTTGAGAACAGAGTCTGACGTGTGTGAAGCTCCTGGTGGAGATGGGGCCCAATGT	921	QY	1743	CGCTGTAGCCCTGTGTGAGCTTGAGCCAGGAGCTTGGCGCCCGCAAGCTCTTACAGGCC	1802
QY	663	GCATGCCGGGCTGCGGGCGCTTCTTCCAGAGGGCCAAAGGACTTGTCTTTTATTTTCGG	722	Db	2002	CGCTGTAGCCCTGTGTGAGCTTGAGCCAGGAGCTTGGCGCCCGCAAGCTCTTACAGGCC	2061
Db	922	GCATGCCGGGCTGCGGGCGCTTCTTCCAGAGGGCCAAAGGACTTGTCTTTTATTTTCGG	981	QY	1803	CAATGCCACAGAGTCAAGTGCAGGCCATGAGGAGGACAGGAGGCAACGGGGCCCA	1862
QY	723	TGAGTACCCCTCTCTTTTGGCCGCTTGCAACAAGCAGTGGGATGTGTAAAGCTACCTCCT	782	Db	2062	CAATGCCACAGAGTCAAGTGCAGGCCATGAGGAGGACAGGAGGCAACGGGGCCCA	2121
Db	982	TGAGTACCCCTCTCTTTTGGCCGCTTGCAACAAGCAGTGGGATGTGTAAAGCTACCTCCT	1041	QY	1863	GTACAGGGGTATCTTGGAAGCCTCTTGTGAGCTCTTCAAATTCACCATCGGATGCGCGCA	1922
QY	783	GGAGAACCCACACAGCCCGCAGCTGCAAGGCCACTGACTCCAGGGCAACACAGTCCCT	842	Db	2122	GTACAGGGGTATCTTGGAAGCCTCTTGTGAGCTCTTCAAATTCACCATCGGATGCGCGCA	2181
Db	1042	GGAGAACCCACACAGCCCGCAGCTGCAAGGCCACTGACTCCAGGGCAACACAGTCCCT	1101	QY	1923	GCTGCGCTTCCAGGAGCAGCTGCACCTCCCGCGCATGTGTGCTGCTGTGTCGCTTA	1982
QY	843	GCATGCCCTAGTATGATCTCGACCAACTCAGCTGAGAACATTTGCACTGGTGACACAGCAT	902	Db	2182	GCTGCGCTTCCAGGAGCAGCTGCACCTCCCGCGCATGTGTGCTGCTGTGTCGCTTA	2241
Db	1102	GCATGCCCTAGTATGATCTCGACCAACTCAGCTGAGAACATTTGCACTGGTGACACAGCAT	1161	QY	1983	CGTGTGCTCACTACATCTCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACCTT	2042
QY	903	GTATGATGGGCTCTTCCAACTGGGGCCCGCTCTGCTTACCGTGCAGCTTGAGACAT	962	Db	2242	CGTGTGCTCACTACATCTCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACCTT	2301
Db	1162	GTATGATGGGCTCTTCCAACTGGGGCCCGCTCTGCTTACCGTGCAGCTTGAGGACAT	1221	QY	2043	CAACAGTGTGCGCACTGCAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCTT	2102
QY	963	CCGCAACTGCAGGATCTCAGGCTCTGAAGCTGGCGGCCCAAGAGGGCAAGATCGAGAT	1022	Db	2302	CAACAGTGTGCGCACTGCAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCTT	2361
Db	1222	CCGCAACTGCAGGATCTCAGGCTCTGAAGCTGGCGGCCCAAGAGGGCAAGATCGAGAT	1281	QY	2103	GGAGATGGAGAAATGGCTATTGTGTGTGAGGAAGAGCAGCGGGCAGGTGTGTGTGAC	2162
QY	1023	TTTTCAGGCACATCTGCAAGCGGAGTTTTCAGGACTGAGGCCACTTTTCCCGAAAGTTTCA	1082	Db	2362	GGAGATGGAGAAATGGCTATTGTGTGTGAGGAAGAGCAGCGGGCAGGTGTGTGTGAC	2421
Db	1282	TTTTCAGGCACATCTGCAAGCGGAGTTTTCAGGACTGAGGCCACTTTTCCCGAAAGTTTCA	1341	QY	2163	CGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGGTCTTCAGGGTGTGAGGAGGT	2222
QY	1083	CGAGTGTGTATGGGCTGTGCGGGTGTGCTGTATGACCTGGCTTCTGTGACACAGCTG	1142	Db	2422	CGTTGGCACTAAGCCAGATGGCAGCCCGGATGAGCGCTGGTCTTCAGGGTGTGAGGAGGT	2481
Db	1342	CGAGTGTGTATGGGCTGTGCGGGTGTGCTGTATGACCTGGCTTCTGTGACACAGCTG	1401	QY	2223	GAACTGGGCTTCAATGGGAGCAGACGCTGCTTACGCTGTGTGAGGACCCGTTCAGGGGCAAG	2282
QY	1143	TGAGGAACTCAGTGTGAGATCATTTGCTTTTCAATGCAAGGCCCGCCAGCCAGCACCG	1202	Db	2482	GAACTGGGCTTCAATGGGAGCAGACGCTGCTTACGCTGTGTGAGGACCCGTTCAGGGGCAAG	2541
Db	1402	TGAGGAACTCAGTGTGAGATCATTTGCTTTTCAATGCAAGGCCCGCCAGCCAGCACCG	1461	QY	2283	TGTCTTCGAACTCTCGAAACCCCTGTCTTGGCTTCCCTTCCCAAGAGGATGAGGATGG	2342
QY	1203	AATGGTCTTTTGGAGCCCTGAAACAACTGTCTGAGCGGAAATGGGATCTGTCTATCCC	1262	Db	2542	TGTCTTCGAACTCTCGAAACCCCTGTCTTGGCTTCCCTTCCCAAGAGGATGAGGATGG	2601
Db	1462	AATGGTCTTTTGGAGCCCTGAAACAACTGTCTGAGCGGAAATGGGATCTGTCTATCCC	1521	QY	2343	TGCTCTGAGGAAACTATGTGCCCTCCAGCTCTTCCAGTCCAACTGATGGGCCAGATG	2402
QY	1263	CAAGTCTTCTTAAACTTCTGTGTAACTGTATGTATCATGTTTCAACGCTGTGTGC	1322	Db	2602	TGCTCTGAGGAAACTATGTGCCCTCCAGCTCTTCCAGTCTTCCAGTCTTATGATGGGCCAGATG	2661
Db	1522	CAAGTCTTCTTAAACTTCTGTGTAACTGTATGTATCATGTTTCAACGCTGTGTGC	1581	QY	2403	CAGCAGAGGCCAGAGGACAGAGCAGAGGATCTTTTCCAAACCACTCTGCTGGCTTGGGG	2462
QY	1323	CTACCATCAGCCTTGAAGAGCAGGCGGCCCTCACCTGAAAGCGGAGGTTGGAAA	1382				

Db	1938	CTGCTTTACTATACAGTGGCTTCAGACACAGGATCTACAGTGTCAATGATCCAGAA	1997
Qy	1683	GGTCATCTCGGGACCTGCTGGCTTCCTTCTGATCTACTAGTCTTCTTTCCTGGCTT	1742
Db	1998	GGTCATCTCGGGACCTGCTGGCTTCCTTCTGATCTACTAGTCTTCTTTCCTGGCTT	2057
Qy	1743	CGCTGAGCCCTGGTGTAGCCCTGAGCCGACGAGGCTTGGCGGCCCGAAGCTCCTACAGGCC	1802
Db	2058	CGCTGAGCCCTGGTGTAGCCCTGAGCCGACGAGGCTTGGCGGCCCGAAGCTCCTACAGGCC	2117
Qy	1803	CAATGCCACAGAGTCACTGAGCCCTGAGGAGGACAGGAGGACAGGGCAACGGGGCCCA	1862
Db	2118	CAATGCCACAGAGTCACTGAGCCCTGAGGAGGACAGGAGGACAGGGCAACGGGGCCCA	2177
Qy	1863	GTACAGGGGTATCCTGGAAGCCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGCGGA	1922
Db	2178	GTACAGGGGTATCCTGGAAGCCTCTTGGAGCTCTTCAAAATTCACCATCGGCATGGCGGA	2237
Qy	1923	GCTGGCCTTCAGAGGAGCTGCACTTCCCGGAGTGGTCTGCTGCTGCTGCTGCTGCTGCTG	1982
Db	2238	GCTGGCCTTCAGAGGAGCTGCACTTCCCGGAGTGGTCTGCTGCTGCTGCTGCTGCTGCTG	2297
Qy	1983	CGTGTCTCACTACATCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGGACCGGT	2042
Db	2298	CGTGTCTCACTACATCTGCTGCTCAACATGCTCATCGCCCTCATGAGCGGACCGGT	2357
Qy	2043	CAACAGTGTCCGCACTGACAGCTGGAGCATCTGGAAAGCTGCAGAAAGCCATCTCTGTCT	2102
Db	2358	CAACAGTGTCCGCACTGACAGCTGGAGCATCTGGAAAGCTGCAGAAAGCCATCTCTGTCT	2417
Qy	2103	GGAGATGGAGAAATGGCTATTGGTGGTCCAGAGAGAGCAGCGGCGAGGTGTGATGCTGAC	2162
Db	2418	GGAGATGGAGAAATGGCTATTGGTGGTCCAGAGAGAGCAGCGGCGAGGTGTGATGCTGAC	2477
Qy	2163	CGTTGGCACAATAGCCAGATGGCAGCGGATGAGCGTGTGCTTCAAGGCTGAGGAGGT	2222
Db	2478	CGTTGGCACAATAGCCAGATGGCAGCGGATGAGCGTGTGCTTCAAGGCTGAGGAGGT	2537
Qy	2223	GAATGGGCTTCATGGAGCAGACGCTGCTCACTGCTGTGTGTGAGGACCCGTCAGGGGCGAG	2282
Db	2538	GAATGGGCTTCATGGAGCAGACGCTGCTCACTGCTGTGTGTGAGGACCCGTCAGGGGCGAG	2597
Qy	2283	TGTCCTCGAACTCTCGAGAACCTGTCTGGCTTCCCTCCCAAGAGGATGAGGATGG	2342
Db	2598	TGTCCTCGAACTCTCGAGAACCTGTCTGGCTTCCCTCCCAAGAGGATGAGGATGG	2657
Qy	2343	TGCTCTGAGAGAAACTATGTGCCGCTCCAGCTCCTCAGTCCCACTGATGGGCCAGATG	2402
Db	2658	TGCTCTGAGAGAAACTATGTGCCGCTCCAGCTCCTCAGTCCCACTGATGGGCCAGATG	2717
Qy	2403	CAGCAGAGGCCAGAGGACAGAGAGGATCTTTTCAACCAATCTGTGCTGTGGCTGTGGG	2462
Db	2718	CAGCAGAGGCCAGAGGACAGAGAGGATCTTTTCAACCAATCTGTGCTGTGGCTGTGGG	2777
Qy	2463	TCCAGT 2469	
Db	2778	TCCAGT 2784	
RESULT 5	A94121		
LOCUS	A94121	2783 bp	DNA
DEFINITION	Sequence 1 from Patent EP0953638.		circular PAT 26-JAN-2000
ACCESSION	A94121		
VERSION	A94121.1	GI:6778849	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 2783)		
	Renard, S. and Partisetti, M.		

TITLE	Human vanilloid receptor-like cation channel		
JOURNAL	Patent: EP 0953638-A 1 03-NOV-1999;		
SYNTHELABO (FR)			
FEATURES	Location/Qualifiers		
source	1..2783		
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3'UTR	2650..2783		
ORIGIN			
Query Match	99.0%; Score 2444.6; DB 6; Length 2783;		
Best Local Similarity	99.7%; Pred. No. 0;		
Matches 2460; Conservative	0; Mismatches 4; Indels 3; Gaps 1;		
Qy	3	CGAGCGCGAGCGCAGCTGGGAGGAGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG	62
Db	267	CAACACCGCGCAGCTGGGAGGAGAGACAGGACCCCTTGACATCTCCATCTGCACAGAGG	326
Qy	63	TCCTGGCTGGACCGAGCAGCTCCTCCTCTTAGGATGACCTCACCTCCAGCTCTCCAGT	122
Db	327	TCCTGGCTGGACCGAGCAGCTCCTCCTCTTAGGATGACCTCACCTCCAGCTCTCCAGT	386
Qy	123	TTTCAGGTTGGAGACATTAGATGGAGGCCAAGAAGATGGCTCTGAGCGGACAGAGGAAA	182
Db	387	TTTCAGGTTGGAGACATTAGATGGAGGCCAAGAAGATGGCTCTGAGCGGACAGAGGAAA	446
Qy	183	GCTGATTTTGGAGCGGGCTGCTCCCATGGAGTACAGTTCCAGGGCGAGAACCGGAA	242
Db	447	GCTGATTTTGGAGCGGGCTGCTCCCATGGAGTACAGTTCCAGGGCGAGAACCGGAA	506
Qy	243	ATTTCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAAGGGAACAGGTGCCAGTCAGCC	302
Db	507	ATTTCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAAGGGAACAGGTGCCAGTCAGCC	566
Qy	303	GGATCCAAACCGATTTCACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCCGA	362
Db	567	GGATCCAAACCGATTTCACCGAGATCGGCTCTTCAATGCGGTCTCCCGGGGTGTCCCCGA	626
Qy	363	GGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACAGCAGTACCTCACCGACTCGGA	422
Db	627	GGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACAGCAGTACCTCACCGACTCGGA	686
Qy	423	ATACACAGAGGGCTCCACAGGTAAGACGTGCCTGTGATGAAGGCTGTGCTGAACCTTAAGGA	482

KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1. Renard, S. and Partiseti, M.	
AUTHORS	A human vanilloid receptor-like cation channel	
TITLE	Patent: WO 9946377-A 1 16-SEP-1999;	
JOURNAL	SANOPI SYNTHELABO (FR); RENARD STEPHANE (FR); PARTISETI MICHEL (FR)	
FEATURES	Location/Qualifiers	
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	Best Local Similarity 99.7%; Pred. No. 0;	
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DB	267 CAACACCGACGCGCAGCTGGAGGAAAGACAGGACCCTTGACATCTCCATCTGCACAGAGG 326	1047 GGAGAACCAACACACCGCCGAGCCTGCAGGCACTGACTCCAGGGCAACACAGCTCCT 1106
QY	63 TCCTGGCTGACCGAGAGCCTCTCTCTCTAGATGACCTCAACCTCCAGCTCTCCAGT 122	843 GCATGCCCTTAGTGATGATCTCGGACAACTCAGCTGAGAACATTGTCACCTGGTACCAGCAT 902
DB	327 TCCTGGCTGACCGAGAGCCTCTCTCTCTAGATGACCTCAACCTCCAGCTCTCCAGT 386	1107 GCATGCCCTTAGTGATGATCTCGGACAACTCAGCTGAGAACATTGTCACCTGGTACCAGCAT 1166
QY	123 TTTTCAGGTTGGAGACATTAGATGAGGCCCAAGAGATGGCTCTGAGCGGACAGAGGAAA 182	903 GTATGATGGGCTCTCTCCAAAGCTGGGGCCGCTCTGCTCCCTACCGTGCAGCTTGAGAGCAT 962
DB	387 TTTTCAGGTTGGAGACATTAGATGAGGCCCAAGAGATGGCTCTGAGCGGACAGAGGAAA 446	1167 GTATGATGGGCTCTCTCCAAAGCTGGGGCCGCTCTGCTCCCTACCGTGCAGCTTGAGAGCAT 1226
QY	183 GCTGGATTTTGGAGCGGGCTGCTCCATGAGTGCACAGTTCACGGCGGAGGACCGGAA 242	963 CGCAACCTGCAGGATCTCAACGCTCTGAAGCTTGCGCGCAAGAGGGGCAAGATCCAGAT 1022
DB	447 GCTGGATTTTGGAGCGGGCTGCTCCATGAGTGCACAGTTCACGGCGGAGGACCGGAA 506	1227 CGCAACCTGCAGGATCTCAACGCTCTGAAGCTTGCGCGCAAGAGGGGCAAGATCCAGAT 1286
QY	243 ATTGCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAGGGAAACAGGTGCCAGTACGC 302	1023 TTTTCAGGACATCTCTGCAGCGGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTAC 1082
DB	507 ATTGCGCCCTCAGATAAGAGTCAACCTCAACTACCGAAGGGAAACAGGTGCCAGTACGC 566	1287 TTTTCAGGACATCTCTGCAGCGGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTAC 1346
QY	303 GGATCCAAACCGATTGACCGAGATGGCTCTTCAATGCGGTCTCCCGGGGTGTCGCCGA 362	1083 CGAGTGGTGTATGGGCTGTCCGGGTGTGCTGTATGACTGTGGCTTCTGTGACAGCTG 1142
DB	567 GGATCCAAACCGATTGACCGAGATGGCTCTTCAATGCGGTCTCCCGGGGTGTCGCCGA 626	1347 CGAGTGGTGTATGGGCTGTCCGGGTGTGCTGTATGACTGTGGCTTCTGTGACAGCTG 1406
QY	363 GGATCTGGCTGGACTTCCAGAGTACCTGAGCAAGACCAGCAAGTACCTCACCGACTCGGA 686	1143 TGAGGAGAACTCAGTGTGGAGATCATTCGCTTTTCAATGCAAGAGCCGACCGACACCG 1202
DB	423 ATACACAGAGGGCTCCACAGGTAAGAGCTGCTGATGAAGGCTGTGCTGAACCTTAAGGA 482	1407 TGAGGAGAACTCAGTGTGGAGATCATTCGCTTTTCAATGCAAGAGCCGACCGACACCG 1466
QY	687 ATACACAGAGGGCTCCACAGGTAAGAGCTGCTGATGAAGGCTGTGCTGAACCTTAAGGA 746	1203 AATGSGTCGTTTTGGAGCGCCCTGAAACAACTGCTGCAGGCGAAATGGGATCTGCTCATCCC 1262
QY	483 CGGAGTCAATGCTGCAATCTGCGACTGCTGCAGATCGACAGGAGCTCTGGCAATCTCA 542	1467 AATGSGTCGTTTTGGAGCGCCCTGAAACAACTGCTGCAGGCGAAATGGGATCTGCTCATCCC 1526
DB	747 CGGAGTCAATGCTGCAATCTGCGACTGCTGCAAGTGCAGAGTGCAGGAGCTCTGGCAATCTCA 806	1263 CAAATGTCCTTAAACTCTGTGTAACTGTGATCTACATGTTCACTTCACGCTGTGGC 1322
QY	543 GCCCCTGGTAAATGCCAGTGCACAGATGACTTATACCGAGGCGCACAGCGCTCTGCACAT 602	1527 CAAATGTCCTTAAACTCTGTGTAACTGTGATCTACATGTTCACTTCACGCTGTGGC 1586
DB	807 GCCCCTGGTAAATGCCAGTGCACAGATGACTTATACCGAGGCGCACAGCGCTCTGCACAT 866	1323 CTACCATCAGCTACCTCGAAGACAGGCGCCCTCACCTCGAAGCGGAGTTGGA 1382
QY	603 CGCATTTGAGAAGAGGATCTGAGTGTGAAAGCTCTGGTGAGATGGGGCCCAATGT 662	1587 CTACCATCAGCTACCTCGAAGACAGGCGCCCTCACCTCGAAGCGGAGTTGGA 1643
DB	867 CGCATTTGAGAAGAGGATCTGAGTGTGAAAGCTCTGGTGAGATGGGGCCCAATGT 926	1383 CTCCATGCTGCTGAGCGGCCACATCCTTATCTCTGCTAGGGGGATCTACCTCTCGTGG 1442
QY	663 GCATGCCCGGGCTGCGGGCGCTTTCTTCAGAGGGGCAAGGAGCTTGCTTTTATTTCCG 722	1644 CTCCATGCTGCTGAGCGGCCACATCCTTATCTCTGCTAGGGGGATCTACCTCTCGTGG 1703
DB	927 GCATGCCCGGGCTGCGGGCGCTTTCTTCAGAGGGGCAAGGAGCTTGCTTTTATTTCCG 986	1443 CCAGCTGTGGTACTTCTGCGGGCGCACGCTGTTCATCTGGATCTCGTTCATGACAGCTA 1502
QY	723 TGAGCTACCCCTCTCTTTTGGCCGCTTGACCAAGCAGTGGGATGTGTGTAAGCTACCTCCT 782	1704 CCAGCTGTGGTACTTCTGCGCGGCCACGCTGTTCATCTGGATCTCGTTCATGACAGCTA 1763
DB	987 TGAGCTACCCCTCTCTTTTGGCCGCTTGACCAAGCAGTGGGATGTGTGTAAGCTACCTCCT 1046	1503 CTTTGAATCCCTCTTCTCTGTTCCAGGCGCTGCTCAAGTGTGTCCAGGTGCTGTGTT 1562

Db	2124	GTACAGGGGTATCTCTGGAAGCCTCTCTGGAGCTCTTCAAAATTCACCATGGCATGGCGGA	2183		
Qy	1923	GCTTGGCTTCCAGAGAGAGCTGCACATTCGCGGCATGGTGTCTGTCTGTCTGCCTTA	1982		
Db	2184	GCTTGGCTTCCAGAGAGAGCTGCACATTCGCGGCATGGTGTCTGTCTGTCTGTCTGCCTTA	2243		
Qy	1983	CGTGTCTCTCACCTTACATCTCTGTCTGTCTCAACATGTCTCATGCCCTCATGAGCGAGACCGT	2042		
Db	2244	CGTGTCTCTCACCTTACATCTCTGTCTGTCTCAACATGTCTCATGCCCTCATGAGCGAGACCGT	2303		
Qy	2043	CAACAGTGTCCCACTGACAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCTCT	2102		
Db	2304	CAACAGTGTCCCACTGACAGCTGGAGCATCTGGAAGCTGCAGAAAGCCATCTCTGTCTCT	2363		
Qy	2103	GGAGATGGAGAAATGGCTATTGGTGGTGCAGGAAGAGCAGCGGGCAGGTGTGATGCTGAC	2162		
Db	2364	GGAGATGGAGAAATGGCTATTGGTGGTGCAGGAAGAGCAGCGGGCAGGTGTGATGCTGAC	2423		
Qy	2163	CGTTGGCACTAAGCAGATGCGAGCGCGGATGAGCGTGTGTCTTCAAGGTGAGAGAGGT	2222		
Db	2424	CGTTGGCACTAAGCAGATGCGAGCGCGGATGAGCGTGTGTCTTCAAGGTGAGAGAGGT	2483		
Qy	2223	GAATCGGGCTTCATGGAGCAGAGCGCTGCCTACGCTGTGTGAGGACCCGTTCAGGGCGAGG	2282		
Db	2484	GAATCGGGCTTCATGGAGCAGAGCGCTGCCTACGCTGTGTGAGGACCCGTTCAGGGCGAGG	2543		
Qy	2283	TGTCCTCTCGAATCTCTCGAAGAACCTGTCTGGCTTCCCTCCCAAGAGGATGAGGATGG	2342		
Db	2544	TGTCCTCTCGAATCTCTCGAAGAACCTGTCTGGCTTCCCTCCCAAGAGGATGAGGATGG	2603		
Qy	2343	TGCTCTGAGGAAAACTATGTGCGCGCTCCAGCTCTCTCCAGTCCAACTGATGGCCACAGTG	2402		
Db	2604	TGCTCTGAGGAAAACTATGTGCGCGCTCCAGCTCTCTCCAGTCCAACTGATGGCCACAGTG	2663		
Qy	2403	CAGCAGGAGGCGCAGGAGCAGAGGAGGATCTTCCAAACACATCTGTCTGGCTCTGGGG	2462		
Db	2664	CAGCAGGAGGCGCAGGAGCAGAGGAGGATCTTCCAAACACATCTGTCTGGCTCTGGGG	2723		
Qy	2463	TCCAGT 2469			
Db	2724	TCCAGT 2730			
RESULT 7	BD251411	2765 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD251411	Ion channel, in particular, vanilloid receptor-like (VR-L) receptor.			
DEFINITION	BD251411	Ion channel, in particular, vanilloid receptor-like (VR-L) receptor.			
ACCESSION	BD251411.1	GI:33061181			
VERSION	JP 2002538768-A/1.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 2765)				
JOURNAL	Garcia, R., Wood, J.N. and England, S.				
COMMENT	Ion channel, in particular, vanilloid receptor-like (VR-L) receptor				
	Patent: JP 2002538768-A 1 19-NOV-2002;				
	UNIVERSITY COLLEGE LONDON				
	OS Homo sapiens (human)				
	PN JP 2002538768-A/1				
	PD 19-NOV-2002				
	PF 08-OCT-1999 JP 2000576011				
	PR 08-OCT-1998 GB 9822124.5				
	PI REYNALDO GARCIA, JOHN NICHOLAS WOOD, STEVEN ENGLAND PC				
	C12N15/09, A01K67/027, A61K31/711, A61K45/00, A61K48/00, A61P29/00, PC				
	A61P37/02,				
	PC C07K14/705, C07K16/28, C12N5/10, C12Q1/02, C12Q1/68, G01N33/15, PC				
	G01N33/50,				
	PC G01N33/53, G01N33/566, C12N15/00, C12N5/00				
	CC n is a or g or c or t				
	FH Key	Location/Qualifiers			

FEATURES	source	misc_feature (2352)	misc_feature (2357)	misc_feature (2475)	Location/Qualifiers
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ORIGIN					
Query Match	98.4%;	Score 2428.8;	DB 6;	Length 2765;	
Best Local Similarity	99.0%;	Pred. No. 0;			
Matches 2442;	Conservative 0;	Mismatches 25;	Indels 0;	Gaps 0;	
Qy	3	CGAGGCCGACGCGCAGCTGGAGAGAGCAGAGCCCTTGACATCTCCATCTGCACAGAGG	62		
Db	264	CAACACCGACGCGCAGCTGGAGAGAGCAGAGCCCTTGACATCTCCATCTGCACAGAGG	323		
Qy	63	TCTGGCTGGACCGAGCAGCTCTCTCTCTAGGATGACCTCACCTCCAGCTCTCCAGT	122		
Db	324	TCTGGCTGGACCGAGCAGCTCTCTCTCTAGGATGACCTCACCTCCAGCTCTCCAGT	383		
Qy	123	TTTCAGTTGGAGACATTAGATGGAGCCCAAGAGATGCTCTGAGGCGGACAGAGGAAA	182		
Db	384	TTTCAGTTGGAGACATTAGATGGAGCCCAAGAGATGCTCTGAGGCGGACAGAGGAAA	443		
Qy	183	GCTGGATTTGGAGCGGCTGCTCCCATGGAGTCAACAGTTCCAGGGGAGGACCGGAA	242		
Db	444	GCTGGATTTGGAGCGGCTGCTCCCATGGAGTCAACAGTTCCAGGGGAGGACCGGAA	503		
Qy	243	ATTGCGCCCTCAGATAAGAGTCAACCTCACTACCGAAAGGGAACAGGTGCCAGTCCAGCC	302		
Db	504	ATTGCGCCCTCAGATAAGAGTCAACCTCACTACCGAAAGGGAACAGGTGCCAGTCCAGCC	563		
Qy	303	GGATCCAAACCGATTGACCGAGATCGGCTCTTCAATGGGTCTCCCGGGGTGCCCCGA	362		
Db	564	GGATCCAAACCGATTGACCGAGATCGGCTCTTCAATGGGTCTCCCGGGGTGCCCCGA	623		
Qy	363	GGATCTGGTGGACTTCCAGAGTACCTGAGCAAGACAGCAAGTACCTCACCGACTCGGA	422		
Db	624	GGATCTGGTGGACTTCCAGAGTACCTGAGCAAGACAGCAAGTACCTCACCGACTCGGA	683		
Qy	423	ATACACAGAGGGCTCCACAGGTAAAGACGTGCTGTGATGAAGGTGTGCTGAACCTTAAGGA	482		
Db	684	ATACACAGAGGGCTCCACAGGTAAAGACGTGCTGTGATGAAGGTGTGCTGAACCTTAAGGA	743		
Qy	483	CGAGTCAATGCTGCTGCTTCCAGTGTGCTGAGTCCAGAGTCCAGGAGCTCTGGCAATCTCA	542		
Db	744	CGGGGTCAATGCTGCTTCCAGTGTGCTGAGTCCAGAGTCCAGGAGCTCTGGCAATCTCA	803		
Qy	543	GCCCTCTGTAATGCGCAGTGCACAGTACTATTACCGAGGCGACAGCGCTCTGCACAT	602		
Db	804	GCCCTCTGTAATGCGCAGTGCACAGTACTATTACCGAGGCGACAGCGCTCTGCACAT	863		
Qy	603	CGCCATTGAGAGAGAGGAGTGTGAGTGTGAGTCTCTGGTGGAGAAATGGGGCCAAATGT	662		
Db	864	CGCCATTGAGAGAGAGGAGTGTGAGTGTGAGTCTCTGGTGGAGAAATGGGGCCAAATGT	923		
Qy	663	GCATGCCGGGCGCTGCGGCGCTTCTCCAGAGGGCCAAAGGAGCTTGTCTTTTATTTTCGG	722		
Db	924	GCATGCCGGGCGCTGCGGCGCTTCTTCCAGAAATGGGCAAGGGAGCTTGTCTTTTATTTGG	983		
Qy	723	TGAGCTACCCCTCTCTTTGGCGCTTGCACCAAGCAGTGGGATGTGTAAGCTACCTCCT	782		
Db	984	TGAGCTACCCCTCTCTTTGGCGCTTGCACCAAGCAGTGGGATGTGTAAGCTACCTCCT	1043		
Qy	783	GGAGAACCCACACAGCCCGCCAGCTGCGAGGCGCACTGACTCCAGGGCAACACAGTCTCT	842		
Db	1044	GGAGAACCCACACAGCCCGCCAGCTGCGAGGCGCACTGACTCCAGGGCAACACAGTCTCT	1103		
Qy	843	GCATGCCCTTAGTGTGATGATCTCGGACAACTCAGCTGAGAAATTCGACTGTGACCAAGAT	902		
Db	1104	GCATGCCCTTAGTGTGATGATCTCGGACAACTCAGCTGAGAAATTCGACTGTGACCAAGAT	1163		

QY	903	GTATGATGGGCTCCTCCAAAGCTGGGGCCCGCCCTCTGCCCCTACCGTGCAGGCTTGAGACAT	962
Db	1164	GTATGATGGGCTCCTCCAAAGCTGGGGCCCGCCCTCTGCCCCTACCGTGCAGGCTTGAGACAT	1223
QY	963	CCGCAACTCAGGATCTCAGCGCTCTGAAGCTGGCCGCCCAAGGAGGCAAGATCGAGAT	1022
Db	1224	CCGCAACTCAGGATCTCAGCGCTCTGAAGCTGGCCGCCCAAGGAGGCAAGATCGAGAT	1283
QY	1023	TTTTCAGGCACATCCTTCAGCGGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTTCA	1082
Db	1284	TTTTCAGGCACATCCTTCAGCGGGAGTTTTCAGGACTGAGCCACCTTTTCCCGAAAGTTTCA	1343
QY	1083	CGAGTGGTGTATGGGCTGTGCGGGTGTGCTGTATGACCTGGCTTCTGTGACAGCTG	1142
Db	1344	CGAGTGGTGTATGGGCTGTGCGGGTGTGCTGTATGACCTGGCTTCTGTGACAGCTG	1403
QY	1143	TGAGGGAACCTCAGTGTCTGAGATCAATTGCTTTTTCATTGCAAGAGCCCGCACGACACCG	1202
Db	1404	TGAGGGAACCTCAGTGTCTGAGATCAATTGCTTTTTCATTGCAAGAGCCCGCACGACACCG	1463
QY	1203	AATGGTGGTTTTCAGGCCCCCTGAAACAACTGCTGCGAGCGGAAATGGGATCTGCTCATCCC	1262
Db	1464	AATGGTGGTTTTCAGGCCCCCTGAAACAACTGCTGCGAGCGGAAATGGGATCTGCTCATCCC	1523
QY	1263	CAAGTCTCTTAAACTTCTGTTGTAATCTGATCTACATGTTTCACTTCAACCGCTGTTC	1322
Db	1524	CAAGTCTCTTAAACTTCTGTTGTAATCTGATCTACATGTTTCACTTCAACCGCTGTTC	1583
QY	1323	CTACCATCAGCTACCTCTGAAGAGCAGGCGCGCCCTCACCTGCAAGCGGAGGTTGGAAA	1382
Db	1584	CTACCATCAGCTACCTCTGAAGAGCAGGCGCGCCCTCACCTGCAAGCGGAGGTTGGAAA	1643
QY	1383	CTCCATGCTGCTGACGGGCGACATCTCTTATCTGCTAGGGGGGATCTACCTCTCGTGGG	1442
Db	1644	CTCCATGCTGCTGACGGGCGACATCTCTTATCTGCTAGGGGGGATCTACCTCTCGTGGG	1703
QY	1443	CGAGCTGTGTACTTCTGGGGGGCGCACGTGTTTCATCTGGATCTCGTTTATAGACAGCTA	1502
Db	1704	CGAATCTGTGTACTTCTGGGGGGCGCACGTGTTTCATCTGGATCTCGTTTATAGACAGCTA	1763
QY	1503	CTTTGAAATCCTCTCTCTGTTTCAGGCGCTGCTCACAGTGGTGTCCAGAGTGTGTGTTT	1562
Db	1764	CTTTGAAATCCTCTCTCTGTTTCAGTCCCTGCTCACAGTGGTGTCCCTGGTGTGTGTTT	1823
QY	1563	CCTGGCCATCGAGTGTACCTGCCCTGCTTGTGTCTGCGCTGGTGTGGGCTGGCTGAA	1622
Db	1824	CCTGGTTCATCGAGTGTGTACCTGCCCTGCTTGTGTCTGCGCTGGTGTGGGCTGGCTGAA	1883
QY	1623	CCTGCTTTACTATACAGTGGCTTCAGGACACAGGATCTACAGTGTATGATCCAGAA	1682
Db	1884	CCTGCTTTACTATACAGTGGCTTCCAGGACACAGGATCTACAGTGTATGATCCAGAA	1943
QY	1683	GGTATCCTCGGGACCTGCTGGCTTCTTCTGATCTACTTACTTCTTCTTCTTCTTCTTCTT	1742
Db	1944	GGTATCCTCGGGACATGTGTGCTTCTTGTGATCTACTTACTTCTTCTTCTTCTTCTTCTT	2003
QY	1743	CGCTGTAGCCCTTGTGTAGCCCTGAGCCAGGAGGCTTGGCGCCCCGAAAGCTCCTACAGGCC	1802
Db	2004	CGCTGTAGCCCTTGTGTAGCCCTGAGCCAGGAGGCTTGGCGCCCCGAAAGCTCCTACAGGCC	2063
QY	1803	CAATGCCACAGAGTCACTGACGCCATGGAGGGACAGGAGGACAGGGGCAACGGGGCCCA	1862
Db	2064	CAATGCCACAGAGTCACTGACGCCATGGAGGGACAGGAGGACAGGGGCAACGGGGCCCA	2123
QY	1863	GTAAGGGGTATCCTTGAAGCCTCTTGGAGCTCTTCAAAATTCACCAATTCGGCATGGCGA	1922
Db	2124	GTAAGGGGTATCCTTGAAGCCTCTTGGAGCTCTTCAAAATTCACCAATTCGGCATGGCGA	2183
QY	1923	GCTGGCTTCCAGGACAGTGTCACTTCCCGGCGATGGTGTCTGTCTGTCTGTCTGTCTGT	1982
Db	2184	GCTGGCTTCCAGGACAGTGTCACTTCCCGGCGATGGTGTCTGTCTGTCTGTCTGTCTGT	2243
QY	1983	CGTGTGCTCCTACCTACATCTCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACCT	2042
Db	2244	CGTGTGCTCCTACCTACATCTCTGCTCAACATGCTCATCGCCCTCATGAGCGAGACCT	2303
QY	2043	CAACAGTGTGCGCACTGACAGCTGGAGCATCTTGGAACTGCGAAGCCATCTTGTCTCT	2102
Db	2304	CAACAGTGTGCGCACTGACAGCTGGAGCATCTTGGAACTGCGAAGCCATCTTGTCTCT	2363
QY	2103	GGAGATGGAGAAATGGCTATTGGTGTGCAAGAAAGCAGCGGGCGAGGTGTGATGCTGAC	2162
Db	2364	GGAGATGGAGAAATGGCTATTGGTGTGCAAGAAAGCAGCGGGCGAGGTGTGATGCTGAC	2423
QY	2163	CGTGTGCACTAAGCCAGATGGCAGCCCGATCAGCGCTGCTGCTTTCAGGCTGGAGAGT	2222
Db	2424	CGTGTGCACTAAGCCAGATGGCAGCCCGATCAGCGCTGCTGCTTTCAGGCTGGAGAGT	2483
QY	2223	GAACTGGGCTTTCATGGGAGCAGACGCTGCTACGCTGTGTGAGGACCCCTCAGGGGCGAG	2282
Db	2484	GAACTGGGCTTTCATGGGAGCAGACGCTGCTACGCTGTGTGAGGACCCCTCAGGGGCGAG	2543
QY	2283	TGTCCCTCGAACTCTCGAGAACCTTGTCTGTGCTTCCCTCCCAAGGAGGATGAGATGG	2342
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ACCESSION			
AX023769 AX023795			
VERSION			
AX023769.1 GI:10184127			
KEYWORDS			
SOURCE			
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ORGANISM			
Homo sapiens			
REFERENCE			
1			
England, S., Wood, J.N. and Garcia, R.			
Ion channels, in particular vanilloid receptor - like (vr-1)			
AUTHORS			
TITLE			
JOURNAL			
Patent: WO 0022121-A 1 20-APR-2000;			
UNIV LONDON (GB) ; ENGLAND STEVEN (GB) ; WOOD JOHN NICHOLAS (GB) ;			
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DEFINITION Sequence 1 from patent US 644440.
ACCESSION AR225700
VERSION AR225700.1 GI:27263801
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2805)
AUTHORS Young, P.E. and Ruben, S.M.
TITLE Vanilloid receptor-2
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 complete cds.

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VERSION	AF129112.1	Best Local Similarity	100.0%;	Pred. No. 0;			
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1 (bases 1 to 2397)						
AUTHORS	Caterina, M.J., Rosen, T.A., Tominaga, M., Brake, A.J. and Julius, D.						
TITLE	A capsaicin-receptor homologue with a high threshold for noxious heat						
JOURNAL	Nature 398 (6726), 436-441 (1999)						
MEDLINE	99215558						
PUBMED	10201375						
REFERENCE	2 (bases 1 to 2397)						
AUTHORS	Caterina, M.J., Rosen, T.A., Tominaga, M., Brake, A.J. and Julius, D.						
TITLE	Direct Submission						
JOURNAL	Submitted (17-FEB-1999) Cellular and Molecular Pharmacology, University of California, 513 Parnassus, San Francisco, CA 94143, USA						
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Query Match	96.4%;	Score 2379.4;	DB 9;	Length 2397;			
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QY	138	ATTAGATGGAGGCCAAGAAGTGGCTCTGAGCGCGGACAGAGAAAGCTGGAATTTGGGAG	197				
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QY	258	AAGAGTCAACCTCACTACCGAAGGGAACAGGTGCCAGTCAGCGGATCCAAACCGATT	317				
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QY	858	GATCTCGGCAACTCAGCTGAGAACATTCAGCTGGTGACAGCATGTATGATGGGCTCCT	917
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LOCUS Sequence 35 from patent US 6335180.
DEFINITION

ACCESSION ARI181402
VERSION ARI181402.1 GI:20223616
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2380)
AUTHORS Julius,D.J., Caterina,M.J. and Brake,A.J.
TITLE Nucleic acid sequences encoding capsaicin receptor and uses thereof
JOURNAL Patent: US 6335180-A 35 01-JAN-2002;
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Best Local Similarity 100.0%; Pred. No. 0;
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QY 139 TTAGATGGAGGCCAAGAGATGGCTCTGAGCGGACAGAGGAAAGCTGGATTTTGGGAGC 198
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QY 199 GGGCTGCT 258
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QY 619 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 678
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Qy	499	ATTCTGCCACTCTGCAGATCGACAGGGACTCTGCGCAATCTCAGCCCTCGTAAATGCC	558	
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Qy	739	TTGGCCGCTTTGACCAAGCAGTGGGATGTGTAAGCTACCTCTGGAGAACCCACACAG	798	
Db	661	TTGGCCGCTTTGACCAAGCAGTGGGATGTGTAAGCTACCTCTGGAGAACCCACACAG	720	
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DEFINITION Sequence 1 from Patent WO9937765.
ACCESSION AX019706
VERSION AX019706.1 GI:10043549
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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Duckworth, D.M., Davis, J.B. and Hayes, P.D.
Human vanilloid receptor homologues
Patent: WO 9937765-A 1 29-JUL-1999;
SMITHKLINE BEECHAM PLC (GB)
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QY 213 GGAGTCAAGTTCCAGGCGGAGGACCGGAATTCGCCCTCCAGATAAGAGTCAACCTCAA 272
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2013	Qy	CATGCTCATCGCCCTCATAGAGCAGACCGTCAACAGTGTCCGCCACTGACAGCTGGAGCAT	2072
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2253	Qy	TAGCCTGTGTGAGGACCCGCTCAGGGCAGGTGTCCCTCGAACTCTCGAGAACCTGTGCTCT	2312
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2221	Db	GGCTTCCCTCCCAAGGAGATGAGGATGTGTGCTCTGAGGAAAATATATGTGCCCGTCCA	2280
2373	Qy	GCTCTCCAGTCCAACTGATGGCCAGATCGACGAGAGGCGCAGAGGACAGAGCAGAGGA	2432
2281	Db	GCTCTCCAGTCCAACTGATGGCCAGATCGACGAGAGGCGCAGAGGACAGAGCAGAGGA	2340
2433	Qy	TCCTTCCAAACC 2443	
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Search completed: October 6, 2005, 20:51:42
Job time : 10366 secs

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814	DB		
721	DB	GGCCACTGACTCCCAAGGCAACACACAGTCTCGATGCCCCCTAGTGTATGATCTCGGACAACATC	780
722	DB		
873	QY	AGCTGAGAAACATTGCACTGGTGACACAGCAATGATATGATGGGCTCCTCCAAGCTGGGGCCCG	932
874	DB		
781	DB	AGCTGAGAAACATTGCACTGGTGACACAGCAATGATATGATGGGCTCCTCCAAGCTGGGGCCCG	840
782	DB		
933	QY	CCTCTGCCCTACCGTGCGAGCTGTGAGACATCATCGCAACCTGCAAGGATCTCACGCTCTGAA	992
934	DB		
841	DB	CCTCTGCCCTACCGTGCGAGCTGTGAGACATCATCGCAACCTGCAAGGATCTCACGCTCTGAA	900
842	DB		
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1621	DB	TCTGATCTACTTACTTCTTTTTCGGGCTTCGCTGTATGCCCTTGGTGTAGCCCTGTAGCCAGGA	1680
1622	DB		
1773	QY	GGCTTGGGCCCCGAAAGCTCCTCAGAGCCCAATGCCACAGAGTCAAGTGCAGGCCCATGGA	1832
1774	DB		
1681	DB	GGCTTGGGCCCCGAAAGCTCCTCAGAGCCCAATGCCACAGAGTCAAGTGCAGGCCCATGGA	1740
1682	DB		

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